

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:32:41 ; Search time 19.3721 Seconds
(without alignments)
84.435 Million cell updates/sec

Title: US-09-020-393b-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFNDVTRLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	128	1 RWHU59	surface glycoprotein
2	63	65.6	126	2 I36914	CD59 protein - bab
3	63	65.6	128	2 I36894	CD59 protein - gre
4	46.5	48.4	1302	2 T20767	hypothetical prote
5	46.5	48.4	1767	2 T20766	hypothetical prote
6	46	47.9	284	2 E83557	probable transcrip
7	46	47.9	777	2 E83748	hypothetical prote
8	45	46.9	706	2 AB0022	probable membrane
9	45	46.9	1307	2 T21283	hypothetical prote
10	44	45.8	205	2 D71639	NADH2 dehydrogenas
11	44	45.8	807	2 D69102	collagenase - Meth
12	43	44.8	544	2 S41626	spike protein chai
13	42	43.8	365	2 T20652	hypothetical prote
14	42	43.8	419	2 C83681	ABC transporter (s
15	42	43.8	434	2 A81326	hypothetical prote
16	42	43.8	434	2 A81697	hypothetical prote
17	42	43.8	464	2 T16889	hypothetical prote
18	41	42.7	117	2 C69969	hypothetical prote
19	41	42.7	179	2 S23358	H ₂ -transporting tw
20	41	42.7	223	1 VCBVCA	coat protein - tob
21	41	42.7	265	2 S64938	hypothetical prote
22	41	42.7	410	2 T51212	related to integra
23	41	42.7	720	2 T38647	hypothetical prote
24	41	42.7	742	2 T23226	hypothetical prote
25	41	42.7	805	2 C88628	protein W03G1.4 [i
26	41	42.7	805	2 C88037	protein K02E7.3 [i
27	41	42.7	805	2 T03896	hypothetical prote
28	41	42.7	906	2 T48898	disease resistance
29	41	42.7	908	2 T48899	disease resistance

30	41	42.7	1162	2 S14940	E2 glycoprotein pr
31	41	42.7	1162	2 S14939	E2 glycoprotein pr
32	41	42.7	1162	2 S07421	E2 glycoprotein pr
33	41	42.7	1217	2 D88996	protein C17B7.7 [i
34	41	42.7	1528	2 S13743	DNA strand transfe
35	41	42.7	1646	1 WMTMS2	186K protein - cuc
36	41	42.7	3433	1 S28381	utrophin - human
37	40	41.7	78	2 H84010	hypothetical prote
38	40	41.7	165	2 A97759	16S rRNA processin
39	40	41.7	165	2 F71691	hypothetical prote
40	40	41.7	218	2 F69972	probable membrane
41	40	41.7	244	2 T00825	probable heat choc
42	40	41.7	398	2 AH0482	conserved hypothet
43	40	41.7	497	2 T06727	hypothetical prote
44	40	41.7	607	2 T43222	meiosis specific p
45	40	41.7	742	1 A43344	synaptic vesicle p

ALIGNMENTS

RESULT 1

RWHU59

surface glycoprotein CD59 precursor [validated] - human

N:Alternate names: 1P5 antigen protein; 20K homologous restriction factor (HRP20); CD59
Plex inhibition factor (MACIF); membrane inhibitor of reactive lysis (MIRL); protectin

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1990 #sequence, revision 30-Sep-1990 #text_change 09-Jul-2004

C/Accession: A46252; J010109; A33405; J00134; A34587; S05504; S09201; A60828; PL0041; A60

R:Petranka, J.G.; Fleenor, D.E.; Sykes, K.; Kaufman, R.E.; Rosse, W.F.

Proc. Natl. Acad. Sci. U.S.A. 89, 7876-7879, 1992

A>Title: Structure of the CD59-encoding gene: further evidence of a relationship to muri

A/Reference number: A46252; MUID:92390353; PMID:1381503

A/Accession: A46252

A/Molecule type: DNA

A/Residues: 1-128 <P&T>

A/Cross-references: UNIPROT:P13987; GB:M84349; GB:M82840; NID:G180149; PIDN:AAA88793.1;

R: Davies, A.; Simmons, D.L.; Hale, G.; Harrison, R.A.; Tighe, N.; Hideshima, T.; Takizawa, H.; Kondo, J.

J. Exp. Med. 170, 637-654, 1989

A>Title: CD59, an LY-6-like protein expressed in human lymphoid cells, regulates the act

A/Reference number: J010109; MUID:89361238; PMID:2475570

A/Accession: J010109

A/Molecule type: mRNA

A/Residues: 1-128 <DAV>

A/Cross-references: EMBL:X16447; NID:G29805; PIDN:CAA34467.1; PID:G29806

R:Okada, H.; Nagami, Y.; Takahashi, K.; Okada, N.; Hideshima, T.; Takizawa, H.; Kondo, J.

Biochem. Biophys. Res. Commun. 162, 1553-1559, 1989

A>Title: 20 KDa homologous restriction factor of complement resembles T cell activating

A/Reference number: A33405; MUID:89350983; PMID:2475111

A/Accession: A33405

A/Molecule type: mRNA

A/Residues: 1-128 <OKA>

A/Cross-references: GB:M27909; NID:G623406; PIDN:AAA60543.1; PID:G623407

R:Sugita, Y.; Tobe, T.; Oda, E.; Tomita, M.; Yasukawa, K.; Yamaji, N.; Takemoto, T.; Fur

J. Biochem. 106, 555-557, 1989

A>Title: Molecular cloning and characterization of MACIF, an inhibitor of membrane chann

A/Reference number: J00134; MUID:90110046; PMID:2606909

A/Accession: J00134

A/Molecule type: mRNA

A/Residues: 1-128 <SUG>

A>Note: parts of this sequence, including the amino end of the mature protein, were conf

A>Note: sites for glycosylation and the absence of glycosylation were confirmed

R:Sawada, R.; Ohashi, K.; Anaguchi, H.; Okazaki, H.; Hattori, M.; Minato, N.; Naruto, M.

DNA Cell Biol. 9, 213-220, 1990

A>Title: Isolation and expression of the full-length cDNA encoding CD59 antigen of human

A/Reference number: A34587; MUID:90253615; PMID:1692709

A/Accession: A34587

A/Molecule type: mRNA

A/Residues: 1-128 <SAW>

A/Cross-references: GB:M34671; NID:G180152; PIDN:AAA51952.1; PID:G180153

R:Sawada, R.; Ohashi, K.; Okano, K.; Hattori, M.; Minato, N.; Naruto, M.

Nucleic Acids Res. 17, 6728, 1989

A;Title: Complementary DNA sequence and deduced peptide sequence for CD59/MEM-43 antigen
A;Reference number: S05504; MUID:89386002; PMID:2476718
A;Accession: S05504
A;Molecule type: mRNA
A;Residues: 27-128 <SA2>
A;Cross-references: EMBL:X15861; NID:g29803; PIDN:CAA33870.1; PID:g1340180
R;Philbrick, W.M.; Pallfree, R.G.E.; Maher, S.E.; Bridgett, M.M.; Sirlin, S.; Bothwell, A
Eur. J. Immunol. 20, 87-92, 1990
A;Title: The CD59 antigen is a structural homologue of murine Ly-6 antigens but lacks in
A;Reference number: S09201; MUID:90168959; PMID:1689664
A;Accession: S09201
A;Molecule type: mRNA
A;Residues: 1-128 <PHI>
A;Cross-references: EMBL:X17198; NID:g29814; PIDN:CAA35059.1; PID:g29815
R;Gabral, A.R.; Cole, L.A.; Walz, D.A.; Castor, C.W.
Arthritis Rheum. 30, 1393-1400, 1987
A;Title: Connective tissue activation. XXXII. Structural and biologic characteristics of
A;Reference number: A60828; MUID:88134429; PMID:3124861
A;Accession: A60828
A;Molecule type: protein
A;Residues: 26-27,'V',29-30,'D',32-37,'X',39-42,'XX',45-50,'X',52-62,'VXRLID' <CAB>
A;Experimental source: normal urine
A;Note: the six unknown or mismatched residues in the amino-terminal fragment correspond
nal fragment was determined by a kinetic carboxypeptidase Y method
R;Stefanova, I.; Hilgert, I.; Kristofova, H.; Brown, R.; Low, M.G.; Horejsi, V.
Mol. Immunol. 26, 153-161, 1989
A;Title: Characterization of a broadly expressed human leucocyte surface antigen MEM-43
A;Reference number: PL0041; MUID:89143489; PMID:2918859
A;Accession: PL0041
A;Molecule type: protein
A;Residues: 26-42 <STE>
R;Harada, R.; Okada, N.; Fujita, T.; Okada, H.
J. Immunol. 144, 1823-1828, 1990
A;Title: Purification of 1F5 antigen that prevents complement attack on homologous cell
A;Reference number: A60774; MUID:90171576; PMID:2307842
A;Accession: A60774
A;Molecule type: protein
A;Residues: 26-42,'XX',45-50,'X',52,'X',54-57,'X',59-63 <HAR>
R;Ninomiya, H.; Stewart, B.H.; Rollins, S.A.; Zhao, J.; Bothwell, A.L.M.; Sims, P.J.
J. Biol. Chem. 267, 8404-8410, 1992
A;Title: Contribution of the N-linked carbohydrate of erythrocyte antigen CD59 to its co
A;Reference number: A38089; MUID:92235085; PMID:1373727
A;Accession: A38089
A;Molecule type: protein
A;Residues: 40-42,'X',44-49 <NIN>
R;Sugita, Y.; Nakano, Y.; Oda, E.; Noda, K.; Tobe, T.; Miura, N.H.; Tomita, M.
J. Biochem. 114, 473-477, 1993
A;Title: Determination of carboxyl-terminal residue and disulfide bonds of MACIF(CD59).
A;Reference number: PX0068; MUID:94103166; PMID:8276756
A;Accession: PX0068
A;Molecule type: protein
A;Residues: 26-29;30-39;40-42,'X',44-48;49-52;56-65;65-72;88-90;92-96 <SU2>
R;Tone, M.; Walsh, L.A.; Waldmann, H.
J. Mol. Biol. 227, 971-976, 1992
A;Title: Gene structure of human CD59 and demonstration that discrete mRNAs are generate
A;Reference number: I37223; MUID:93021133; PMID:1383553
A;Accession: I37223
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-128 <RES>
A;Cross-references: EMBL:Z14113; NID:g29810; PIDN:CAA78486.1; PID:g825637
C;Comment: This cell surface antigenic glycoprotein inhibits homologous complement lysis
g the binding of C9 and C8 to C5b
C;Comment: This glycosylphosphatidylinositol-anchored protein is deficient in cases of p
C;Genetics:
A;Gene: GDB:CD59
A;Cross-references: GDB:119769; OMIM:107271
A;Map position: 11p13-11p13
A;Introns: 23/1; 57/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; membrane protein; phosphatid
F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-102/Product: surface glycoprotein CD59 #status experimental <MAT>
F;26-102/Domain: Ly-6 homology <LY6>
F;103-128/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;28-51,31-38,44-64/Disulfide bonds: #status experimental
F;33/Binding site: carbohydrate (Asn) (covalent) #status absent
F;43/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;70-88,89-94/Disulfide bonds: (or 70-89, 88-94) #status experimental
F;102/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match 100.0%; Score 96; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
|:|||||:|:|:|
Db 67 FEHCNFDVTRLRENE 83

RESULT 2
I36914

C;Species: Papio sp. (baboon)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I36914
R;Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, E.R.; Rother, R
Immunogenetics 41, 51, 1995
A;Title: Primate terminal complement inhibitor homologues of human CD59.
A;Reference number: I36894; MUID:95104908; PMID:7528724
A;Accession: I36914
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-126 <RES>
A;Cross-references: UNIPROT:Q28785; GB:L22862; NID:g5143327; PIDN:AAA74127.1; PID:g5143328
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-100/Domain: Ly-6 homology <LY6>

Query Match 65.6%; Score 63; DB 2; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.0054;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
|:|||||:|:|:|
Db 67 FANCNFNDISTLLKESE 83

RESULT 3
I36894

CD59 protein - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I36894
R;Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, E.R.; Rother, R
Immunogenetics 41, 51, 1995
A;Title: Primate terminal complement inhibitor homologues of human CD59.
A;Reference number: I36894; MUID:95104908; PMID:7528724
A;Accession: I36894
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-128 <RES>
A;Cross-references: UNIPROT:Q28216; GB:L22863; NID:g5143314; PIDN:AAA74126.1; PID:g5143315
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-102/Domain: Ly-6 homology <LY6>

Query Match 65.6%; Score 63; DB 2; Length 128;
Best Local Similarity 58.8%; Pred. No. 0.0055;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
|:|||||:|:|:|
Db 67 FANCNFNDISTLLKESE 83

RESULT 4

A;Residues: 1-284 <STO>
 A;Cross-references: UNIPROT:Q915M0; GB:AE004506; GB:AE004091; NID:G9946584; PIDN:AAG0409
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA0708

Query Match 47.9%; Score 46; DB 2; Length 284;
 Best Local Similarity 60.0%; Pred. No. 7.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCNFNDVTTLRRENE 17
 DB 26 HCVPSNITTLRELE 40

RESULT 7
 E83748
 hypothetical protein BH0789 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: E83748
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: E83748
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-777 <STO>
 A;Cross-references: UNIPROT:Q9KER0; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA8045
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH0789

Query Match 47.9%; Score 46; DB 2; Length 777;
 Best Local Similarity 46.7%; Pred. No. 21;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNCFNDVTTLRRE 15
 DB 136 FKHSNFHDYLTQIKE 150

RESULT 8
 AB0022
 probable membrane protein YPO0174 [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB0022
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AB0022
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-706 <KUD>
 A;Cross-references: UNIPROT:Q82JD9; GB:AL590842; PIDN:CAC89036.1; PID:gl5978277; GSPDB:G
 C;Genetics:
 A;Gene: YPO0174

Query Match 46.9%; Score 45; DB 2; Length 706;
 Best Local Similarity 53.8%; Pred. No. 27;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRLEN 16
 DB 589 CHINEMTTLRLEN 601

RESULT 9

T21283
hypothetical protein F23A7.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21283
R;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19401
A;Accession: T21283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1307 <WIL>
A;Cross-references: UNIPROT:Q93554; EMBL:Z81067; PIDN:CA802976.1; GSPDB:GN00028; CESP:P2
A;Experimental source: clone F23A7
C;Genetics:
A;Gene: CESP:F23A7.5
A;Map position: X
A;Introns: 154/1; 230/2; 271/3; 307/1; 466/2; 551/2; 627/3; 663/1; 699/3; 746/3; 772/3;
Query Match 46.9%; Score 45; DB 2; Length 1307;
Best Local Similarity 69.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 CNFNDVTRLREN 16
Db 654 CKINDPTTLREN 666
RESULT 10
H71639
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J RP790 - *Rickettsia prowazekii*
C;Species: *Rickettsia prowazekii*
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H71639
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, T.
Nature 396, 133-140, 1998
A;Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71639
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-205 <AND>
A;Cross-references: UNIPROT:Q9ZCG3; GB:AJ235273; GB:AJ235269; NID:G3861237; PIDN:CAA1521
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: nuoJ; RP790
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6
C;Keywords: membrane-associated complex; NAD; oxidoreductase
Query Match 45.8%; Score 44; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 NFNDVTRLREN 16
Db 77 NFNQAITKLREN 88
RESULT 11
D69102
collagenase - *Methanobacterium thermoautotrophicum* (strain Delta H)
C;Species: *Methanobacterium thermoautotrophicum*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69102
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69102
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-807 <MTH>
A;Cross-references: UNIPROT:O27791; GB:AE000931; GB:AE000666; NID:G2622885; PIDN:AAB8622
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1763
A;Start codon: TTG
Query Match 45.8%; Score 44; DB 2; Length 807;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 FEHCNFDVTRLRE 15
Db 562 FRECDWVDVRSILRE 576
RESULT 12
S41626
spike protein chain 1 precursor - avian infectious bronchitis virus (fragment)
C;Species: avian infectious bronchitis virus, IBV
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41626
R;Cavanagh, D.; Davis, P.J.
Arch. Virol. 130, 471-476, 1992
A;Title: Sequence analysis of strains of avian infectious bronchitis coronavirus isolated
A;Reference number: S41626
A;Accession: S41626
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-544 <CAV>
A;Cross-references: UNIPROT:Q82667; EMBL:X64737; NID:G453158; PIDN:CAA46003.1; PID:G45315
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992
C;Superfamily: coronavirus E2 glycoprotein
Query Match 44.8%; Score 43; DB 2; Length 544;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HCNFNDVDT 10
Db 101 HCNFTDIT 108
RESULT 13
T20652
hypothetical protein Y102A5C.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20652; T26370
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19305
A;Accession: T20652
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <WIL>
A;Cross-references: UNIPROT:Q9XTF4; EMBL:Z81496; PIDN:CA804075.1; GSPDB:GN00023; CESP:Y10
A;Experimental source: clone F09C6
R;Gardner, A.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z20204
A;Accession: T26370
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <WIL>
A;Cross-references: EMBL:AL031627; PIDN:CAA20972.1; CESP:Y102A5C.1
A;Experimental source: clone Y102A5C
C;Genetics:
A;Gene: CESP:Y102A5C.1
A;Map position: 5
A;Introns: 93/2; 104/1; 298/3
Query Match 43.8%; Score 42; DB 2; Length 365;

Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNPNVDVTRLREN 16
||| | | | | | | |
Db 288 FEHLCFQDVKRLLES 303

RESULT 14
C83681
ABC transporter (substrate-binding protein) BH0251 [imported] - Bacillus halodurans (str
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83681
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83681
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <STO>
A;Cross-references: UNIPROT:Q9KG62; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA039
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0251
C;Superfamily: LIV-binding protein

Query Match 43.8%; Score 42; DB 2; Length 419;
Best Local Similarity 40.0%; Pred. No. 48;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCMFNVDVTRLRENE 17
| : : : : : : : :
Db 219 HTDNTIIRISE 233

RESULT 15
AE1326
Hypothetical protein lmo2013 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Dec-2002
C;Accession: AE1326
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1326
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-434 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00091.1; PID:g16411466; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2013
C;Superfamily: uncharacterized conserved protein

Query Match 43.8%; Score 42; DB 2; Length 434;
Best Local Similarity 52.9%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 FEHCNPNVDVTRLRENE 17
||| | | | | | | |
Db 30 FEKCFNTYTTLOETE 46

Search completed: June 8, 2005, 10:44:57
Job time: 21.3721 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:24:21 ; Search time 89.3488 Seconds
(without alignments)
97.431 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58
Perfect score: 96
Sequence: 1 FEHCNFNDVTRLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	128	1	CD59 HUMAN
2	63	65.6	126	1	CD59_PAPSP
3	63	65.6	128	1	CD59_CERAE
4	63	65.6	128	1	CD59_P3
5	60	62.5	128	2	Q8SP13
6	51.5	53.6	337	2	Q8SQ46
7	51	53.1	935	2	Q7ZNX4
8	49	51.0	124	1	Q6FSB7
9	49	51.0	124	1	CD59_RABIT
10	49	51.0	143	2	Q96676
11	48	50.0	481	2	Q8M824
12	48	50.0	721	2	Q27308
13	47	49.0	128	1	CD59_CALSQ
14	47	49.0	419	2	Q6BZP9
15	47	49.0	721	2	Q8I955
16	46.5	48.4	1302	2	Q7JMA4
17	46.5	48.4	1767	2	Q19346
18	46	47.9	284	2	Q9I5M0
19	46	47.9	338	1	ARGC_LEPIN
20	46	47.9	777	2	Q9KER0
21	46	47.9	934	2	Q8WZU8
22	45	46.9	127	2	Q70527
23	45	46.9	133	2	Q8Q930
24	45	46.9	149	2	Q7TAV1
25	45	46.9	165	2	Q68X25
26	45	46.9	259	2	Q6N828
27	45	46.9	402	2	Q8IL43
28	45	46.9	448	2	Q6BWL4
29	45	46.9	538	2	Q6J1B2
30	45	46.9	548	2	Q913Y3
31	45	46.9	618	2	Q80MT5

32	45	46.9	706	2	Q664N9
33	45	46.9	706	2	Q8ZJD9
34	45	46.9	965	2	Q7Z1J6
35	44	45.8	84	2	Q8MN28
36	44	45.8	133	2	Q918A9
37	44	45.8	136	2	Q918B0
38	44	45.8	205	1	NUOJ_RICPR
39	44	45.8	205	2	Q68V79
40	44	45.8	231	2	Q8IFL1
41	44	45.8	236	2	Q91177
42	44	45.8	275	2	Q8CSS9
43	44	45.8	513	2	Q82618
44	44	45.8	530	2	O55343
45	44	45.8	534	2	Q6J1D9

ALIGNMENTS

RESULT 1

CD59_HUMAN	STANDARD;	PRT;	128 AA.
ID	CD59_HUMAN		
AC	P13987;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (MBM43 antigen) (Protectin) (Membrane inhibitor of reactive lysis) (MIRL) (20 kDa DE homologous restriction factor) (HRF-20) (HRF20) (1F5 antigen).		
GN	Names=CD59;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=T-cell;		
RX	MEDLINE=89361238; PubMed=2475570;		
RA	Davies A., Simmons D.L., Hale G., Harrison R.A., Tighe H., Lachmann P.J., Waldmann H.;		
RA	"CD59, an LY-6-like protein expressed in human lymphoid cells, regulates the action of the complement membrane attack complex on homologous cells.";		
RT	J. Exp. Med. 170:637-654(1989).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90168959; PubMed=1689664;		
RA	Philbrick W.M., Palfree R.G.E., Roger G.E., Maher S.E., Bridgett M.M., Sirlin S., Bothwell A.L.M.;		
RA	"The CD59 antigen is a structural homologue of murine Ly-6 antigens but lacks interferon inducibility.";		
RT	Eur. J. Immunol. 20:87-92(1990).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89350993; PubMed=2475111;		
RA	Okada H., Nagami Y., Takahashi K., Okada N., Hideshima T., Takizawa H., Kondo J.;		
RA	"20 kDa homologous restriction factor of complement resembles T cell activating protein.";		
RT	Biochem. Biophys. Res. Commun. 162:1553-1559(1989).		
RL	[4]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=90110046; PubMed=2606909;		
RX	Sugita Y., Tobe T., Oda E., Tomita M., Yasukawa K., Yamaji N., Takemoto T., Furuichi K., Takayama M., Yano S.;		
RA	"Molecular cloning and characterization of MACIF, an inhibitor of membrane channel formation of complement.";		
RT	J. Biochem. 106:555-557(1989).		
RL	[5]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=90253615; PubMed=1692709;		
RX	Sawada R., Ohashi K., Aneguchi H., Okazaki H., Hattori M., Minato N.,		


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DR EMBL; X17198; CAA35059.1; --
DR EMBL; M34671; AAA51952.1; --

Query Match      100.0%; Score 96; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 4; le-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
   |||||
DB 67 FEHCNFDVTRLRENE 83

RESULT 2
CD59_PAPSP
ID_CD59_PAPSP STANDARD; PRT; 126 AA.
AC Q28785;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Name=CD59;
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP MEDLINE=95104908; PubMed=7528724;
RA Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
RA Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
RT "Primate terminal complement inhibitor homologues of human CD59.";
RL Immunogenetics 41:51-51(1995).
CC -1- FUNCTION: Potent inhibitor of the complement membrane attack
CC complex (MAC) action. Acts at or after the C5b-8 stage of MAC
CC assembly.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC
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CC
CC EMBL; L22862; AAA74127.1; --
CC PIR; I36914; I36914.
CC HSPSP; P13987; LCDS.
CC InterPro; IPR003632; Ly-6 CD59.
CC ProSite; PS00983; Ly6_UPAR.
CC Pfam; PF00021; UPAR_Ly6; 1.
CC ProDom; PD003128; Ly-6_CD59; 1.
CC SMART; SM00134; LU; 1.
CC ProSITE; PS00983; Ly6_UPAR; 1.
CC Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
CC SIGNAL 1 25
CC CHAIN 26 100
CC PROPEP 101 126
CC LIPID 100 100
CC DOMAIN 26 100
CC DISULFID 28 51
CC DISULFID 31 38
CC DISULFID 44 64
CC DISULFID 70 88
CC DISULFID 89 94
CC CARBOHYD 43 43
CC LIPID 100 100
CC SEQUENCE 126 AA; 13716 MW; 7900FF937871EBDC CRC64;

Query Match      100.0%; Score 96; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 4; le-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
   |||||
DB 67 FEHCNFDVTRLRENE 83

RESULT 3
CD59_CERAE
ID_CD59_CERAE STANDARD; PRT; 128 AA.
AC Q28216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Name=CD59;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP MEDLINE=95104908; PubMed=7528724;
RA Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
RA Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
RT "Primate terminal complement inhibitor homologues of human CD59.";
RL Immunogenetics 41:51-51(1995).
CC -1- FUNCTION: Potent inhibitor of the complement membrane attack
CC complex (MAC) action. Acts at or after the C5b-8 stage of MAC
CC assembly.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC
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CC
CC EMBL; L22863; AAA74126.1; --
CC PIR; I36894; I36894.
CC HSPSP; P13987; LCDS.
CC InterPro; IPR003632; Ly-6 CD59.
CC ProSite; PS00983; Ly6_UPAR.
CC Pfam; PF00021; UPAR_Ly6; 1.
CC ProDom; PD003128; Ly-6_CD59; 1.
CC SMART; SM00134; LU; 1.
CC ProSITE; PS00983; Ly6_UPAR; 1.
CC Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
CC SIGNAL 1 25
CC CHAIN 26 102
CC PROPEP 103 128
CC LIPID 102 102
CC DOMAIN 26 108
CC DISULFID 28 51
CC DISULFID 31 38
CC DISULFID 44 64
CC DISULFID 70 88
CC DISULFID 89 94
CC CARBOHYD 43 43
CC SEQUENCE 128 AA; 14007 MW; 9778DEF7F7F05152 CRC64;

Query Match      65.6%; Score 63; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.014;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
   |||||
DB 67 FANCNFDISTLLKESE 83
```

```
QY 1 FEHCNFDVTVTRLRENE 17
   |::|::|::|::|::|
Db 67 FANCNFDISTLKESE 83

RESULT 4
Q8SPI3 Q8SPI3 PRELIMINARY; PRT; 128 AA.
AC Q8SPI3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CD59 antigen p18-20 allele B.
GN Name=CD59;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain parietal lobe;
RA Osada N., Kusuda J., Hirata M., Tanuma R., Hida M., Sugano S.,
RA Hirai M., Hashimoto K.;
RT "Search for genes positively selected during primate evolution by 5'-
RT end-sequence screening of cynomolgus monkey cDNAs.";
RL Genomics 79:657-662(2002).
DR EMBL; AB072018; BAB86807.1; -.
DR HSSP; P13987; ICDS.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1_CD59; 1.
DR PROSITE; PS00983; LY6_UPAR; 1.
DR PROSITE; PS00983; LY6_UPAR; 1.
SQ SEQUENCE 128 AA; 13958 MW; 997639A9C93F6E52 CRC64;

Query Match 65.6%; Score 63; DB 2; Length 128;
Best Local Similarity 58.8%; Pred. No. 0.014;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTRLRENE 17
   |::|::|::|::|::|
Db 67 FANCNFDISTLKESE 83

RESULT 5
Q8SQ46 Q8SQ46 PRELIMINARY; PRT; 128 AA.
AC Q8SQ46;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CD59 antigen p18-20 allele A.
GN Name=CD59;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Medulla oblongata;
RA Osada N., Kusuda J., Hirata M., Tanuma R., Hida M., Sugano S.,
RA Hirai M., Hashimoto K.;
RT "Search for genes positively selected during primate evolution by 5'-
RT end-sequence screening of cynomolgus monkey cDNAs.";
RL Genomics 79:657-662(2002).
DR EMBL; AB072017; BAB86806.1; -.
DR HSSP; P13987; ICDS.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6_UPAR.
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DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6_UPAR; 1.
SQ SEQUENCE 128 AA; 14008 MW; 8867D956D63F6E52 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 128;
Best Local Similarity 52.9%; Pred. No. 0.046;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTRLRENE 17
   |::|::|::|::|::|
Db 67 FANCNFDISTLKESE 83

RESULT 6
Q7ZNX4 Q7ZNX4 PRELIMINARY; PRT; 337 AA.
AC Q7ZNX4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00NE091;
RA Mamadou S., Montavon C., Ben A., Djilo A., Rabiou S., Mboup S.,
RA Delaporte E., Peeters M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ429913; CAD22673.1; -.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR GO; GO:0019028; C-viral capsid; IEA.
DR GO; GO:0019031; C-viral envelope; IEA.
DR GO; GO:0005198; F-structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 337
SQ SEQUENCE 337 AA; 37267 MW; 854D18511C94C99F CRC64;

Query Match 53.6%; Score 51.5; DB 2; Length 337;
Best Local Similarity 58.8%; Pred. No. 3.5;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 FEHCNFDVTVTRLRENE 17
   |::|::|::|::|::|
Db 30 FKNCSEF-VTTELDRNK 45

RESULT 7
Q6FSB7 Q6FSB7 PRELIMINARY; PRT; 935 AA.
AC Q6FSB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P40355 Saccharomyces cerevisiae YJR061w.
GN ORFNames=CAGL0H01793g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
```

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA Swenne D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Boucher P., Souciet J.L.;
RT "Genome evolution in yeasts";
RT Nature 430:35-44(2004)
DR EMBL; CR380954; CAG59810.1; -- 5051C3B01DDB647F CRC64;
SQ SEQUENCE 935 AA; 110737 MW; 110737 MW; CEA64C816772CABD CRC64;
Query Match 53.1%; Score 51; DB 2; Length 935;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 FEHCNFNDVTRLRENE 17
| : : : : :
DB 613 FNQDNFDDLSRVNNE 629
RESULT 8
ID CD59 RABIT STANDARD; PRT; 124 AA.
AC 077541;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Name=CD59;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-64.
RX TISSUE=Erythrocyte, and Lymphocytes;
RX MEDLINE=98221206; PubMed=9553129; DOI=10.1074/jbc.273.17.10665;
RA Zhao X.-J., Zhao J., Zhou Q., Sims P.J.;
RT "Identity of the residues responsible for the species-restricted
RT complement inhibitory function of human CD59.";
RL J. Biol. Chem. 273:10665-10671(1998).
CC -|- FUNCTION: Potent inhibitor of the complement membrane attack
CC complex (MAC) action. Acts by binding to the C8 and/or C9
CC components of the assembling MAC, thereby preventing
CC incorporation of the multiple copies of C9 required for complete
CC formation of the osmolytic pore.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -|- MISCELLANEOUS: The mature form of this CD59 contains an additional
CC serine residue before the conserved N-terminal leucine residue
CC found in all other CD59 homologs sequenced to date.
CC -|- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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CC
CC EMBL; AF040387; AAC23590.1; --
CC HSPSP; P13987; 1ERG.
CC InterPro; IPR003632; LY-6_CD59.
CC Pfam; PF00021; UPAR_Ly6; 1.
CC
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CC
CC EMBL; L22861; AAA35372.1; --
CC HSPSP; P13987; LCDS
CC InterPro; IPR003632; LY-6_CD59.
CC Pfam; PF00021; UPAR_Ly6; 1.
CC ProDom; PD003128; LY-6_CD59; 1.
CC SMART; SM00134; LU; 1.
CC PROSITE; PS00983; LY6_UPAR; 1.
CC Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.

DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6_UPAR; FALSE_NEG.
KW Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Lipoprotein; Signal.
FT SIGNAL 1 24 CD59 glycoprotein.
FT CHAIN 25 101 Removed in mature form (By similarity).
FT PROPEP 102 124 UPAR/Ly6.
FT DOMAIN 25 101
FT DISULFID 28 51 By similarity.
FT DISULFID 31 38 By similarity.
FT DISULFID 44 64 By similarity.
FT DISULFID 70 88 By similarity.
FT DISULFID 89 94 By similarity.
FT CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT LIPID 101 101 GPI-anchor amidated glycine (By
FT similarity).
SQ SEQUENCE 124 AA; 13870 MW; CEA64C816772CABD CRC64;
Query Match 51.0%; Score 49; DB 1; Length 124;
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 FEHCNFNDVTRLREN 16
| : : : : :
DB 67 YEDCNFEFSNRLEEN 82
RESULT 9
ID CD59 AOTTR STANDARD; PRT; 128 AA.
AC P51447;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Name=CD59;
OS Aotus trivirgatus (Night monkey) (Douroucoul).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104908; PubMed=7528724;
RA Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
RA Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
RT "Primate terminal complement inhibitor homologues of human CD59.";
RL Immunogenetics 41:51-51(1995).
CC -|- FUNCTION: Potent inhibitor of the complement membrane attack
CC complex (MAC) action. Acts at or after the C5b-8 stage of MAC
CC assembly.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -|- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; L22861; AAA35372.1; --
CC HSPSP; P13987; LCDS
CC InterPro; IPR003632; LY-6_CD59.
CC Pfam; PF00021; UPAR_Ly6; 1.
CC ProDom; PD003128; LY-6_CD59; 1.
CC SMART; SM00134; LU; 1.
CC PROSITE; PS00983; LY6_UPAR; 1.
CC Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.

```
FT SIGNAL 1 25 By similarity.
FT CHAIN 26 102 CD59 glycoprotein.
FT PROPEP 103 128 Removed in mature form (By similarity).
FT DOMAIN 26 108 UPAR/Ly6.
FT DISULFID 28 51 By similarity.
FT DISULFID 31 38 By similarity.
FT DISULFID 44 64 By similarity.
FT DISULFID 70 88 By similarity.
FT DISULFID 89 94 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT LIPID 102 102 GPI-anchor amidated asparagine (By similarity).
FT SEQUENCE 128 AA; 14200 MW; 62D19B95589E55B CRC64;

Query Match 51.0%; Score 49; DB 1; Length 128;
Best Local Similarity 52.9%; Pred. No. 3.2;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
DB 67 FEDCTFSRVNQLSENE 83

RESULT 10
Q966T6 PRELIMINARY; PRT; 143 AA.
AC Q966T6;
DT 01-DSC-2001 (TrEMBLrel. 19, Created)
DT 01-DSC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cofilin-2 (Hypothetical protein).
GN Names=DCOF3;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21541281; PubMed=11683919;
RA Aizawa H., Kishi Y., Iida K., Sameshima M., Yahara I.;
RT "Cofilin-2, a novel type of cofilin, is expressed specifically at aggregation stage of Dictyostelium discoideum development.";
RL Genes Cells 6:913-921(2001).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BAB62414.1; -.
DR EMBL; AC116984; AAO51299.1; -.
DR DictyBase; DDB0185192; cofilin.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind coflin.
DR Pfam; PF00241; Cofilin ADF; I.
DR ProDom; PD002129; Actbind_coflin; 1.
DR SMART; SM00102; ADF; 1.
KW Hypothetical protein.
SQ SEQUENCE 143 AA; 16362 MW; A78731198E6F40B2 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 143;
Best Local Similarity 57.1%; Pred. No. 3.7;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 CNFNDVTRLRENE 17
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Db 55 CNFNELTQCFKENE 68

RESULT 11
O8M8Z4 PRELIMINARY; PRT; 481 AA.
ID Q8M8Z4;
AC Q8M8Z4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Maturase (Fragment).
DE Names=matk;
GN Styxax officinalis.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Ericales; Styxaceae; Styxax.
OX NCBI_TaxID=153544;
RN [1];
RP SEQUENCE FROM N.A.
RA Bremer B., Bremer K., Heidari N., Erixon P., Olmstead R.G.,
RA Anderberg A.A., Kallersjö M., Barkhordarian E.;
RT "Phylogenetics of asterids based on 3 coding and 3 non-coding chloroplast DNA markers and the utility of non-coding DNA at higher taxonomic levels.";
RL Mol. Phylogenet. Evol. 24:273-300(2002).
DR EMBL; AJ429300; CAD22196.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR008998; Agglutinin.
DR InterPro; IPR004442; Intron maturase2.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 481 AA; 56836 MW; 2B862PBF8551A60F CRC64;

Query Match 50.0%; Score 48; DB 2; Length 481;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
DB 158 YEHCHWNNFTT 168

RESULT 12
Q27308 PRELIMINARY; PRT; 721 AA.
ID Q27308;
AC Q27308;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 82.
GN Name=hsp82;
OS Anopheles albimanus (New world malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7167;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Santa Tecla;
RX MEDLINE=96209490; PubMed=8630537;
RA Benedict M.Q., Levine B.J., Ke Z.X., Cockburn A.F., Seawright J.A.;
RT "Precise limitation of concerted evolution to ORFs in mosquito Hsp82 genes.";
RL Insect Mol. Biol. 5:73-79(1996).
DR EMBL; L47285; AAB05639.1; -.
DR EMBL; L47285; AAB05638.1; -.
DR HSSP; P07900; I0SF.
DR GO; GO:0005524; F:ATP binding; IEA.
```

DR GO: GO:0051082; F:unfolded protein binding; IEA.
 DR GO: GO:006457; P:protein folding; IEA.
 DR GO: GO:006986; P:response to unfolded protein; IEA.
 DR InterPro: IPR009079; 4 helix cytokine.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR001404; Hsp90.
 DR Pfam: PF02518; HATPase_c; 1.
 DR Pfam: PF00183; HSP90; 1.
 DR PRINTS: PR00775; HEATSHOCK90.
 DR SMART: SM00387; HATPase_c; 1.
 DR PROSITE: PS00298; HSP90; 1.
 KW Heat shock.
 SQ SEQUENCE 721 AA; 82153 MW; C71867C5610452EA CRC64;

Query Match 50.0%; Score 48; DB 2; Length 721;
 Best Local Similarity 43.8%; Pred. No. 31;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EHCNFDVTVTLRENE 17
 ||: || ||: ||: ||:
 Db 455 EYCSLNDYVGEMKENQ 470

RESULT 13

CD59 CALSQ STANDARD; PRT; 128 AA.
 AC P46657;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
 GN Name=CD59;
 OS Callithrix sp. (Marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104908; PubMed=7528724;
 RA Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
 RA Guilmette E.R., Rother R.P., Zavairo G.B., Squinto S.P.;
 RT "Primate terminal complement inhibitor homologues of human CD59.";
 RL Immunogenetics 41:51-51(1995).
 CC -1- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts at or after the C5b-8 stage of MAC assembly.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.

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EMBL: L22860; AAA35398.1; -.
 HSPSP: P13987; ICDS.
 DR InterPro: IPR003632; Ly-6_CD59.
 DR InterPro: IPR001526; Ly6_UPAR.
 DR Pfam: PF00021; UPAR_Ly6; 1.
 DR ProDom: PD003128; Ly-6_CD59; 1.
 DR SMART: SM00134; LU; 1.
 DR PROSITE: PS00983; Ly6_UPAR; 1.
 KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
 FT SIGNAL 1 25 By similarity.
 FT CHAIN 26 102 CD59 glycoprotein.
 FT PROPEP 103 128 Removed in mature form (By similarity).
 FT DOMAIN 26 108 UPAR/Ly6.
 FT DISULFID 28 51 By similarity.

FT DISULFID 31 38 By similarity.
 FT DISULFID 44 64 By similarity.
 FT DISULFID 70 88 By similarity.
 FT DISULFID 89 93 By similarity.
 FT CARBOHYD 43 43 N-linked (GlcNAc...) (potential).
 FT LIPID 102 102 GPI-anchor amidated asparagine (By similarity).
 SQ SEQUENCE 128 AA; 14210 MW; 7A44CCAACDECD4 CRC64;

Query Match 49.0%; Score 47; DB 1; Length 128;
 Best Local Similarity 47.1%; Pred. No. 7;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTLRENE 17
 ||: || ||: ||: ||:
 Db 67 FEDCTFQLSNQLSENE 83

RESULT 14

O6BZR9 PRELIMINARY; PRT; 419 AA.
 AC Q6BZR9;
 DT 25-OCT-2004 (Tremblrel. 28, Created)
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Similar to sp|P40160 Saccharomyces cerevisiae YNL207w.
 GN ORFNames=YAL10F31383g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=284591;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Karsset A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Winkler P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382132; CAG78906.1; -.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000687; RIO1_UNK.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF01163; RIO1; 1.
 DR SMART: SM00090; RIO; 1.
 SQ SEQUENCE 419 AA; 48198 MW; 660EC3BE22EE2622 CRC64;

Query Match 49.0%; Score 47; DB 2; Length 419;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 HCNFNDVTVTLRENE 16
 ||: || ||: ||: ||:
 Db 226 HCDNFNFNIMIREN 239

RESULT 15

Q819S5
ID Q819S5 PRELIMINARY; PRT; 721 AA.
AC Q819S5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsp90.
OS Heterodera glycines (Soybean cyst nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=51029;
RN [1]
RP SEQUENCE FROM N.A.
RA Skantar A.M., Carta L.K.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461150; AAC14563.2; -.
DR HSP; P07900; IYER.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001404; Hsp90.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00183; HSP90; 1.
DR PRINTS; PR00775; HEATSHOCK90.
DR SMART; SM00387; HATPase_c; 1.
DR PROSITE; PS00298; HSP90; 1.
SQ SEQUENCE 721 AA; 82956 MW; 6C4370F357643793 CRC64;

Query Match 49.0%; Score 47; DB 2; Length 721;
Best Local Similarity 43.8%; Pred. No. 46;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EHCNENDVTRLENE 17
Db 459 EPCSFKDYVSRMKNQ 474

Search completed: June 8, 2005, 10:44:04
Job time : 92.3488 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 12:14:04 ; Search time 159 seconds
(without alignments)
41.352 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 47 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	70	5 ABB07534	Abb07534 Amino aci
2	96	100.0	71	5 ABB07537	Abb07537 Recombina
3	96	100.0	77	2 AAY27313	Aay27313 Human CD5
4	96	100.0	77	5 ABB07532	Abb07532 Human sol
5	96	100.0	82	5 ABB07535	Abb07535 Human rec
6	96	100.0	83	5 ABB07536	Abb07536 Human rec
7	96	100.0	88	5 ABB07540	Abb07540 Amino aci
8	96	100.0	99	5 ABB07538	Abb07538 Amino aci
9	96	100.0	100	5 ABB07539	Abb07539 Amino aci
10	96	100.0	102	2 AAW09041	Aaw09041 Human mem
11	96	100.0	103	2 AAR11426	Aar11426 Human lym
12	96	100.0	103	2 AAR32291	Aar32291 Sequence
13	96	100.0	105	5 AAMS0629	Aam50629 Human CD5
14	96	100.0	107	2 AAR02039	Aar02039 Human mem
15	96	100.0	115	3 AAG03766	Aag03766 Human sec
16	96	100.0	115	3 AAG03765	Aag03765 Human sec
17	96	100.0	115	3 AAG03764	Aag03764 Human sec
18	96	100.0	126	8 ADO41946	Ado41946 Human com
19	96	100.0	127	2 AAY27311	Aay27311 Human CD5
20	96	100.0	128	2 AAR04704	Aar04704 Sequence
21	96	100.0	128	2 AAR07444	Aar07444 Human mem
22	96	100.0	128	2 AAR11876	Aar11876 Human lym
23	96	100.0	128	2 AAR80240	Aar80240 Human mem
24	96	100.0	128	2 AAR86315	Aar86315 Human CD5
25	96	100.0	128	2 AAW26318	Aaw26318 Human CD5

26	96	100.0	128	4 AAU00688	Aau00688 Human CD5
27	96	100.0	128	7 ADA50041	Ada50041 Human CD5
28	96	100.0	128	7 ADD25548	Add25548 Binding d
29	96	100.0	128	7 ADES6894	Ade58894 Human Pro
30	96	100.0	128	7 ADD45530	Add45530 Human Pro
31	96	100.0	128	7 ADES6890	Ade58890 Human Pro
32	96	100.0	128	7 ADJ69312	Adj69312 Human hea
33	96	100.0	128	7 ADL91008	Adl91008 Human CD5
34	96	100.0	128	7 ADN95931	Adn95931 Human BEC
35	96	100.0	128	8 ADP23084	Adp23084 PRO poly
36	96	100.0	130	8 ABM83101	Abm83101 Human dia
37	96	100.0	190	7 ADE07977	Ade07977 Novel pro
38	96	100.0	260	4 AAU00685	Aau00685 Human CTL
39	96	100.0	260	7 ADA50035	Ada50035 Pig CTIA4
40	96	100.0	260	7 ADL91002	Adl91002 Human CTL
41	96	100.0	261	4 AAU00684	Aau00684 Porcine C
42	96	100.0	261	7 ADA50033	Ada50033 Pig CTIA4
43	96	100.0	261	7 ADL91000	Adl91000 Pig CTIA4
44	96	100.0	270	7 ADA50056	Ada50056 Pig CTIA4
45	96	100.0	271	7 ADA50058	Ada50058 Pig CTIA4
46	96	100.0	330	8 ADO41954	Ado41954 Human CD5
47	96	100.0	334	8 ADO41950	Ado41950 Human CR2

ALIGNMENTS

RESULT 1

ABB07534
ID ABB07534 standard; peptide; 70 AA.

XX ABB07534;

XX 23-APR-2002 (first entry)

DE Amino acid sequence of APT634.

XX CD59; lipid raft derivative; DAP; neuroprotective; nootropic; human;
KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
KW antipruritic; antiasthmatic; dermatological; hypotensive; vasotropic;
KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
KW immunosuppressive; antianemic; nephrotropic; antinfertility;
KW antibacterial; antiatherosclerotic; vulnerary.

OS Homo sapiens.

XX WO200204638-A1.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-GB003034.

XX 07-JUL-2000; 2000GB-00016811.

XX (ADPR-) ADPROTECH LTD.

XX Rowling PJE, Smith GP, Ridley SH;

XX WPI; 2002-164646/21.

PT Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
PT complement regulatory molecule for treating disorders involving
PT complement activity and various inflammatory, neurological and immune
disorders.

XX Example 2; Page 44; 51pp; English.

XX The invention relates to a soluble derivative (I) of a soluble
CC polypeptide. (I) has two or more heterologous membrane binding elements
CC with low membrane affinity covalently associated with the polypeptide,
CC the elements being capable of interacting with components of cellular or
CC artificial membranes exposed to extracellular fluids and target lipid
CC raft components of membrane. (I) is useful for treating disorders

CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
 CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, corneal
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (antibody- or complement-mediated
 CC infertility), and wound healing. The present sequence represents the
 CC amino acid sequence of APT634, used in the synthesis of a lipid raft
 CC targeted derivative of soluble human urinary CD59 (APT637)
 CC
 XX Sequence 70 AA;
 SQ

Query Match 100.0%; Score 96; DB 5; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTRENE 17
 |||||
 Db 42 FEHCNFNDVTTRENE 58

RESULT 2
 ABB07537
 ID ABB07537 standard; peptide; 71 AA.
 AC ABB07537;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Recombinant human CD59 protein with C-terminal cysteine (APT2061).
 XX
 KW CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
 KW antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic;
 KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 KW immunosuppressive; antianemic; nephrotropic; antiinfertility;
 KW antibacterial; antiatherosclerotic; vulnerary.
 XX
 OS Homo sapiens.
 XX
 PN WO200204638-A1.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-GB003034.
 XX
 PR 07-JUL-2000; 2000GB-00016811.
 XX
 XX (ADPR-) ADPROTECH LTD.
 PA
 XX Rowling PJE, Smith GP, Ridley SH;
 PI
 XX WPI; 2002-164646/21.
 DR
 XX
 PT Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders.
 XX
 XX Example 7; Page 45; 51pp; English.
 PS
 XX
 CC The invention relates to a soluble derivative (I) of a soluble
 CC polypeptide. (I) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,

CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
 CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, corneal
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (antibody- or complement-mediated
 CC infertility), and wound healing. The present sequence represents APT2061
 CC which comprises soluble human CD59 and a C-terminal cysteine residue,
 CC recombinantly expressed in chinese hamster ovary cells
 XX
 SQ Sequence 71 AA;
 Query Match 100.0%; Score 96; DB 5; Length 71;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTRENE 17
 |||||
 Db 42 FEHCNFNDVTTRENE 58

RESULT 3
 AAY27313
 ID AAY27313 standard; peptide; 77 AA.
 XX
 AC AAY27313;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 DE Human CD59 protein fragment.
 XX
 KW CD59 mediated complement; human; CD59 protein; C9 protein; mimetic;
 KW tumour therapy; complement-mediated inflammation; immune disorder;
 KW immunovascularitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
 KW plasma membrane antigen.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO9940115-A2.
 XX
 PD 12-AUG-1999.
 XX
 PF 09-FEB-1999; 99WO-US002802.
 XX
 PR 09-FEB-1998; 98US-00020393.
 XX
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX Sims PJ;
 PI
 XX WPI; 1999-527301/44.
 DR
 XX
 PT Compounds modulating CD59 mediated complement activity, for treatment of,
 PT e.g. immunovascularitis.
 XX
 XX Disclosure; Fig 8A-B; 75pp; English.
 PS
 XX
 CC The invention relates to compounds modulating CD59 mediated complement
 CC activity. It provides (i) molecules structurally mimicking human CD59
 CC amino acid residues 42-58 (region which serves as binding site for CD59 -

CC C9 interactions) when they are in a spatial orientation which can inhibit
 CC the formation of the human C5b-9 complex. These mimetics specifically
 CC bind to amino acid residues 359-384 of human C9. (ii) molecules
 CC structurally mimicking C9 amino acids 359-384 when they are in a spatial
 CC orientation which can promote the formation of the C5b-9 complex.
 CC Compounds that mimic CD59 can be used to increase CD59 inhibition of C5b-
 CC 9 complex assembly. This is especially useful in patients in need of
 CC suppression of complement-mediated inflammation, e.g. immune disorders
 CC and diseases such as immunovascularitis, rheumatoid arthritis, scleroderma.
 CC Compounds that mimic C9 can be used to promote C5b-9 complex assembly.
 CC This is useful in patients in need of complement activation. The
 CC composition can be administered as an adjunct to tumour therapy. The
 CC present sequence represents a human CD59 (a plasma membrane antigen)
 CC protein fragment
 XX
 SQ Sequence 77 AA;

Query Match 100.0%; Score 96; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
 |||||
 Db 42 FEHCNFNDVTTTLRENE 58

RESULT 4
 ABB07532
 ID ABB07532 standard; peptide; 77 AA.

AC ABB07532;

XX 23-APR-2002 (first entry)

DT Human soluble CD59 fragment.

DE
 XX CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiatic;
 KW antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic;
 KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 KW immunosuppressive; antianemic; nephrotropic; antiinfertility;
 KW antibacterial; antiatherosclerotic; vulnery.

OS Homo sapiens.

XX WO200204638-A1.

PN 17-JAN-2002.

XX 06-JUL-2001; 2001WO-GB003034.

XX 07-JUL-2000; 2000GB-00016811.

XX (ADPR-) ADPROTECH LTD.

XX Rowling PJE, Smith GP, Ridley SH;

XX WPI; 2002-164646/21.

XX Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders.

XX Example 1; Page 43; Sipp; English.

XX The invention relates to a soluble derivative (I) of a soluble
 CC polypeptide. (I) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other

CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, corneal
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (antibody- or complement-mediated
 CC infertility), and wound healing. The present sequence represents a
 CC fragment of soluble CD59 isolated from human urine. This is used in the
 CC synthesis of a lipid raft targeted derivative of soluble human urinary
 CC CD59 (APT632)
 XX
 SQ Sequence 77 AA;

Query Match 100.0%; Score 96; DB 5; Length 77;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
 |||||
 Db 42 FEHCNFNDVTTTLRENE 58

RESULT 5

ABB07535

ID ABB07535 standard; peptide; 82 AA.

AC ABB07535;

XX 23-APR-2002 (first entry)

DT Human recombinant CD59 protein fragment.

DE
 XX CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiatic;
 KW antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic;
 KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 KW immunosuppressive; antianemic; nephrotropic; antiinfertility;
 KW antibacterial; antiatherosclerotic; vulnery.

OS Homo sapiens.

XX WO200204638-A1.

PN 17-JAN-2002.

XX 06-JUL-2001; 2001WO-GB003034.

XX 07-JUL-2000; 2000GB-00016811.

XX (ADPR-) ADPROTECH LTD.

XX Rowling PJE, Smith GP, Ridley SH;

XX WPI; 2002-164646/21.

XX Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders.

XX Example 6; Page 44; Sipp; English.

XX The invention relates to a soluble derivative (I) of a soluble
 CC polypeptide. (I) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other

CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
 CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, corneal
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (antibody- or complement-mediated
 CC infertility), and wound healing. The present sequence represents a
 CC recombinant human CD59 with a C-terminal cysteine (APT2060)
 XX
 SQ Sequence 82 AA;

Query Match 100.0%; Score 96; DB 5; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
 Db 42 FEHCNFDVTTTLRENE 58
 |||||

RESULT 6
 ABB07536
 ID ABB07536 standard; peptide; 83 AA.
 AC ABB07536;
 DT 23-APR-2002 (first entry)
 XX Human recombinant CD59 protein with C-terminal cysteine (APT635).
 DE
 XX CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
 KW antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic;
 KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 KW immunosuppressive; antianemic; nephrotropic; antiinfertility;
 KW antibacterial; antiatherosclerotic; vulnerary.
 XX
 OS Homo sapiens.
 XX WO200204638-A1.
 PN
 XX 17-JAN-2002.
 PD
 XX 06-JUL-2001; 2001WO-GB003034.
 PF
 XX 07-JUL-2000; 2000GB-00016811.
 PR
 XX (ADPR-) ADPROTECH LTD.
 PA
 XX Rowling PJE, Smith GP, Ridley SH;
 XX WPI; 2002-164646/21.
 XX
 DR
 XX Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders.
 XX
 XX Claim 8; Page 45; 51pp; English.
 PS
 XX The invention relates to a soluble derivative (I) of a soluble
 CC

CC polypeptide. (I) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
 CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, corneal
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (antibody- or complement-mediated
 CC infertility), and wound healing. The present sequence represents APT635
 CC which comprises soluble human CD59 and a C-terminal cysteine residue,
 CC recombinantly expressed in *E. coli*
 XX
 SQ Sequence 83 AA;

Query Match 100.0%; Score 96; DB 5; Length 83;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
 Db 43 FEHCNFDVTTTLRENE 59
 |||||

RESULT 7
 ABB07540
 ID ABB07540 standard; peptide; 88 AA.
 XX AC ABB07540;
 XX 23-APR-2002 (first entry)
 DT
 XX Amino acid sequence of APT2065.
 DE
 XX CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
 KW antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic;
 KW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 KW immunosuppressive; antianemic; nephrotropic; antiinfertility;
 KW antibacterial; antiatherosclerotic; vulnerary.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 71..72
 FT /note= "disulphide bridge"
 FT
 XX WO200204638-A1.
 PN
 XX 17-JAN-2002.
 PD
 XX 06-JUL-2001; 2001WO-GB003034.
 PF
 XX 07-JUL-2000; 2000GB-00016811.
 PR
 XX (ADPR-) ADPROTECH LTD.
 PA
 XX Rowling PJE, Smith GP, Ridley SH;
 XX WPI; 2002-164646/21.
 XX

PT Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
PT complement regulatory molecule for treating disorders involving
PT complement activity and various inflammatory, neurological and immune
PT disorders.

XX Example 8; Page 47; 51pp; English.

XX The invention relates to a soluble derivative (I) of a soluble
XX polypeptide. (I) has two or more heterologous membrane binding elements
XX with low membrane affinity covalently associated with the polypeptide,
XX the elements being capable of interacting with components of cellular or
XX artificial membranes exposed to extracellular fluids and target lipid
XX raft components of membrane. (I) is useful for treating disorders
XX amenable to treatment by a soluble peptide fragment of CD59, DAF or other
XX therapeutic agent, and for the preparation of a medicament for treatment
XX of disorders involving complement activity and various inflammatory and
XX immune disorders. (I) is useful for treating neurological disorders (e.g.
XX multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
XX brain injury and allergic encephalitis), disorders of inappropriate or
XX undesirable complement activation (e.g. xenograft rejection, corneal
XX graft rejection), inflammatory disorders (including ulcerative colitis,
XX Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
XX pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
XX infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
XX infectious diseases or sepsis (e.g. multiple organ failure, septic
XX shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
XX gravis), reproductive disorders (antibody- or complement-mediated
XX infertility), and wound healing. The present sequence represents the
XX amino acid sequence of APT2065

XX Sequence 88 AA;

Query Match 100.0%; Score 96; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 8
ABB07538
ID ABB07538 standard; peptide; 99 AA.
XX ABB07538;
XX 23-APR-2002 (first entry)
XX Amino acid sequence of APT2062.

CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
antipariatic; antiasthmatic; dermatological; hypotensive; vasotropic;
antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
immunosuppressive; antianemic; nephrotropic; antiinfertility;
antibacterial; antiatherosclerotic; vulnerary.

Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers
XX Disulfide-bond 82. .83
XX /note= "disulphide bridge"

WO200204638-A1.
XX 17-JAN-2002.
XX 06-JUL-2001; 2001WO-GB003034.
XX 07-JUL-2000; 2000GB-00016811.

XX (ADPR-) ADPROTECH LTD.
XX Rowling PJE, Smith GP, Ridley SH;
XX WPI; 2002-164646/21.

XX Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
XX complement regulatory molecule for treating disorders involving
XX complement activity and various inflammatory, neurological and immune
XX disorders.

XX Example 8; Page 46; 51pp; English.

XX The invention relates to a soluble derivative (I) of a soluble
XX polypeptide. (I) has two or more heterologous membrane binding elements
XX with low membrane affinity covalently associated with the polypeptide,
XX the elements being capable of interacting with components of cellular or
XX artificial membranes exposed to extracellular fluids and target lipid
XX raft components of membrane. (I) is useful for treating disorders
XX amenable to treatment by a soluble peptide fragment of CD59, DAF or other
XX therapeutic agent, and for the preparation of a medicament for treatment
XX of disorders involving complement activity and various inflammatory and
XX immune disorders. (I) is useful for treating neurological disorders (e.g.
XX multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
XX brain injury and allergic encephalitis), disorders of inappropriate or
XX undesirable complement activation (e.g. xenograft rejection, corneal
XX graft rejection), inflammatory disorders (including ulcerative colitis,
XX Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
XX pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
XX infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
XX infectious diseases or sepsis (e.g. multiple organ failure, septic
XX shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
XX gravis), reproductive disorders (antibody- or complement-mediated
XX infertility), and wound healing. The present sequence represents the
XX amino acid sequence of APT2062

XX Sequence 99 AA;

Query Match 100.0%; Score 96; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 9
ABB07539
ID ABB07539 standard; peptide; 100 AA.
XX ABB07539;
XX 23-APR-2002 (first entry)
XX Amino acid sequence of APT2063.

CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant;
antipariatic; antiasthmatic; dermatological; hypotensive; vasotropic;
antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
immunosuppressive; antianemic; nephrotropic; antiinfertility;
antibacterial; antiatherosclerotic; vulnerary.

Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers
XX Disulfide-bond 83. .84
XX /note= "disulphide bridge"

PN W0200204638-A1.
XX 17-JAN-2002.
XX
XX
XX 06-JUL-2001; 2001W0-GB003034.
XX
XX 07-JUL-2000; 2000GB-00016811.
XX
XX (ADPR-) ADPROTECH LTD.
XX
XX Rowling PJE, Smith GP, Ridley SH;
PI WPI; 2002-164646/21.
XX
XX Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble
PT complement regulatory molecule for treating disorders involving
PT complement activity and various inflammatory, neurological and immune
PT disorders.
XX
XX Claim 8; Page 46; 51pp; English.
XX
XX The invention relates to a soluble derivative (I) of a soluble
CC polypeptide. (I) has two or more heterologous membrane binding elements
CC with low membrane affinity covalently associated with the polypeptide,
CC the elements being capable of interacting with components of cellular or
CC artificial membranes exposed to extracellular fluids and target lipid
CC raft components of membrane. (I) is useful for treating disorders
CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
CC therapeutic agent, and for the preparation of a medicament for treatment
CC of disorders involving complement activity and various inflammatory and
CC immune disorders. (I) is useful for treating neurological disorders (e.g.
CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
CC brain injury and allergic encephalitis), disorders of inappropriate or
CC undesirable complement activation (e.g. xenograft rejection, corneal
CC graft rejection), inflammatory disorders (including ulcerative colitis,
CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
CC infarction, hypertension, renal ischaemia, restenosis, atherosclerosis),
CC infectious diseases or sepsis (e.g. multiple organ failure, septic
CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, haemolytic anaemia, glomerulonephritis and myasthenia
CC gravis), reproductive disorders (antibody- or complement-mediated
CC infertility), and wound healing. The present sequence represents the
CC amino acid sequence of APT2063
XX
XX Sequence 100 AA;
SQ
Query Match 100.0%; Score 96; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTTLRENE 17
Db |||||
43 FEHCNFDVTTTLRENE 59
RESULT 10
AAW09041
ID AAW09041 standard; protein; 102 AA.
XX
AC AAW09041;
XX
XX 23-SEP-1997 (first entry)
DT
XX Human membrane attack complex inhibitory factor mutant Asn18Gln.
DE
XX Human; membrane attack complex; inhibitory factor; MAC1F; mutant;
XX inhibition; complement; mediation; cytotoxicity; bFGF; basic;
KW fibroblast growth factor; suppression; hyperacute; inflammation;
KW transplant rejection.
XX
XX Homo sapiens.
OS
XX WPI; 1991-106290/15.
DR

FH Key Location/Qualifiers
FT Peptide 1..25
FT Peptide /label= sig_peptide
FT Peptide 26..102
FT Misc-difference 43 /label= mat_peptide
FT /note= "wild type Asn replaced by Gln"
XX
XX W09700320-A1.
PN
XX 03-JAN-1997.
PD
XX 13-JUN-1996; 96W0-JP001609.
XX
XX 16-JUN-1995; 95JP-00174282.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
PA
XX Yamaji N, Suzuki H, Egashira A, Yasunaga K, Itou K, Sugita Y;
PI Masuho Y;
PI
XX WPI; 1997-077527/07.
DR N-PSDB; AAT49584.
DR
XX Modified human membrane attack complex inhibitory factor - has glutamine
PT at position 18 and is an antiinflammatory and complement blocker, useful
PT for inhibition of transplant hyper-acute rejection.
XX
XX Claim 1; Page 35; 59pp; Japanese.
XX
XX The present sequence is the human membrane attack complex inhibitory
CC factor (MAC1F) mutant Asn18Gln (residues 1-77), which inhibits complement
CC mediated cytotoxicity, and the release of PGI2 and basic fibroblast growth
CC factor (bFGF) by complement. It can be used to suppress transplanted
CC organ rejection, especially hyperacute transplant rejection, and the non-
CC lethal effects of complement, e.g. inflammation
XX
XX Sequence 102 AA;
SQ
Query Match 100.0%; Score 96; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTTLRENE 17
Db |||||
67 FEHCNFDVTTTLRENE 83
RESULT 11
AAR11426
ID AAR11426 standard; protein; 103 AA.
XX
XX AAR11426;
AC
XX 11-JUN-1991 (first entry)
DT
XX Human lymphocyte surface antigen.
DE
XX lymphocyte; surface antigen; autoimmune disease; cancer.
KW
XX Homo sapiens.
OS
XX JP03048696-A.
PN
XX 01-MAR-1991.
PD
XX 14-JUL-1989; 89JP-00183264.
PF
XX 14-JUL-1989; 89JP-00183264.
PR
XX (TORA) TORAY IND INC.
PA
XX WPI; 1991-106290/15.
DR

DR N-PSDB; AAQ11251.
XX Surface antigen of human lymphocyte - for use in study of human immune
PT system of 101 residues.
XX Claim 1; Page 1; 12pp; Japanese.
XX This protein is similar to the murine lymphocyte antigen Ly 6. Antibodies
CC raised against the antigen can be used in formulations for the treatment
CC of autoimmune diseases, cancer and infections. The corresponding
CC nucleotide sequence does not include an initial Leu codon. See also
XX AAQ11252-4
XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 96; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 12
AAR32291
ID AAR32291 standard; protein; 103 AA.
XX
AC AAR32291;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1993 (first entry)
XX
DE Sequence of CD59.
XX
KW Complement mediated attack inhibitor; CD59; transplant rejection; ss.
XX Homo sapiens.
XX
PN WO9302188-A1.
XX
PD 04-FEB-1993.
XX
PF 14-JUL-1992; 92WO-US005920.
XX
PR 15-JUL-1991; 91US-00729926.
PR 29-JUN-1992; 92US-00906394.
XX
PA (OKLA-) OKLAHOMA MED RES FOUND.
PA (UYIA) UNIV YALE.
XX
PI Sims PJ, Bothwell ALM, Elliot EA, Flavell RA, Madri J, Rollins S;
PI Bell L, Squinto S;
XX
XX
DR WPI; 1993-058786/07.
DR N-PSDB; AAQ36708.
XX
XX Genetically engineered mammalian cell for treatment of coronary artery
PT disease - inhibits complement-mediated attack and does not express
PT surface proteins encoded by class I or II major histocompatibility
PT complex genes.
XX
XX Claim 31; Page 75; 89pp; English.
XX
CC The inventors claim a cell which contains a gene sequence which encodes
CC protein CD59. CD59 is expressed by the cell and CD59 inhibits complement
CC mediated attack of the cell. The cells fail to elicit T lymphocyte
CC mediated attack or are resistant to complement mediated attack. They can
CC be used to treat patients with immune disorders. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 96; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 13
AAM50629
ID AAM50629 standard; protein; 105 AA.
XX
AC AAM50629;
XX
DT 04-APR-2002 (first entry)
XX
DE Human CD59.
XX
KW CD59; protectin; 1F-5Ag; H19; HRF20; MAC1F; M1RL; P-18; human; genomics;
KW evolution; AIDS; HIV.
XX
OS Homo sapiens.
XX
PN WO200196603-A2.
XX
PD 20-DEC-2001.
XX
PF 06-JUN-2001; 2001WO-US018310.
XX
PR 09-JUN-2000; 2000US-00591435.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W, Sikela JM;
XX WPI; 2002-130744/17.
XX
XX Determining human or non-human primate polynucleotide or polypeptide
PT sequences associated with a physiological trait and have undergone
PT evolutionary changes, for therapeutic use, involves using statistical
PT methods.
XX
XX Example 18; Page 85-86; 141pp; English.
XX
XX The present sequence is that of human CD59 (also known as protectin, 1F-
CC 5Ag, H19, HRF20, MAC1F, M1RL and P-18). CD59 acts as one of the
CC inhibitors of membrane attack complexes. HIV virions which have
CC incorporated host cell CD59 are protected from the action of complement.
CC Thus, in humans, HIV uses CD59 to protect itself from attack by the
CC victim's immune system. Comparative evolutionary analysis of the CD59
CC genes of several primate species has revealed that the chimpanzee CD59
CC gene has been subjected to positive selection. While the basic function
CC of CD59 is most likely conserved between chimpanzees and humans, some
CC changes have probably occurred in the orientation of the protein with
CC respect to the cell membrane. This may render the chimpanzee protein (see
CC AAM50630) unusable to the HIV virion. Alternatively, the chimpanzee
CC protein may not be subject to incorporation by the HIV virion.
CC Elucidation of the mechanism can be used to design a therapeutic
CC intervention for infected humans that mimics the chimpanzee resistance to
CC progression to full-blown AIDS. This is an example of the method of the
CC invention in which comparative genomics is used to identify specific gene
CC changes responsible for differences in functions and diseases
CC distinguishing humans from non-humans. Polynucleotide and polypeptide
CC sequences corresponding to evolved traits may be relevant to human
CC diseases or conditions such as unique or enhanced human brain functions,
CC longer human life spans, susceptibility or resistance to disease,
CC including AIDS and cancer, and aesthetic traits such as hair growth
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 96; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTVTLRENE 17
|||||
Db 43 FEHCNFNDVTVTLRENE 59

RESULT 14
AAR80239
ID AAR80239 standard; protein; 107 AA.
XX
AC AAR80239;
XX
DT 25-MAR-2003 (revised)
DT 17-APR-1996 (first entry)
XX
XX Human membrane attack complex inhibition factor.
XX
XX MACIF; membrane attack complex inhibition factor; complement system;
KW regulation; activation; final stage; inhibit damage; disease therapy;
KW type II allergy; type III allergy; inflammatory disease treatment;
KW phosphatidylinositol anchor; glycoprotein; diagnosis.
XX
XX Homo sapiens.
XX

Key Location/Qualifiers
FH Peptide 1..25
FT /label= secretory signal sequence
FT /note= "optionally not present, replaced with H or Met"
FT Protein 26..35
FT /note= "core human MACIF protein"
FT Peptide 96..101
FT /label= PI_attachment_signal_sequence
FT Peptide 101..107
FT /note= "optionally not present"
FT Modified-site 101
FT /label= PI_anchor
FT /note= "modified by PI - skeletal structure composed of
phospho-ethanolamine, glycan and phosphatidylinositol"
FT Peptide 102..107
FT /note= "optionally not present"
XX
XX EP672683-A1.
XX
XX 20-SEP-1995.
XX
XX 19-APR-1990; 95EP-00200379.
XX
XX 21-APR-1989; 89JP-00103088.
XX 12-JUL-1989; 89JP-00179933.
XX 06-SEP-1989; 89JP-00230983.
XX 13-SEP-1989; 89JP-00238246.
XX 21-SEP-1989; 89JP-00247818.
XX 27-OCT-1989; 89JP-00281197.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX Tomita M, Sugita Y, Takemoto T, Furuichi K, Takayama M;
PI Kasukawa K, Yano S, Yamaji N, Ito K;
XX
XX WPI; 1995-321975/42.
XX N-PSDB; AAQ98532.
XX
XX Peptide with human membrane attack complex inhibition factor activity -
PT also DNA and expression vectors used to regulate the complement system in
PT the final stage of complement activation.
XX
XX Claim 2; Page 28; 49pp; English.
XX
XX Human membrane attack complex inhibition factor (MACIF) regulates the
CC complement system in the final stage of complement activation and
CC inhibits damage of human cells and tissues as a result of MAC formation.
CC Naturally occurring human MACIF is a glycoprotein of mol. wt. 18 +/- 1 kDa

CC (by SDS-PAGE) with a phosphatidylinositol (PI) anchor at position 76
CC (Glu) at the C-terminus. When the gene encoding MACIF is expressed in
CC bacteria, the gene (see AAQ98532) gives a modified human MACIF protein
CC comprising 128 amino acid residues (AAR80240); the PI anchor attachment
CC does not occur in that case. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 96; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTVTLRENE 17
|||||
Db 67 FEHCNFNDVTVTLRENE 83

RESULT 15
AAG03766
ID AAG03766 standard; protein; 115 AA.
XX
AC AAG03766;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 7847.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX N-PSDB; AAC03772.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 7847; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 96; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
XX OS Homo sapiens.
XX PN W02004045520-A2.
XX PD 03-JUN-2004.
XX PF 13-NOV-2003; 2003WO-US036459.
XX PR 15-NOV-2002; 2002US-0426676P.
XX PA (MUSC-) MUSC FOUND RES DEV.
XX PI Tomlinson S;
XX DR WPI; 2004-420518/39.
XX DR N-PSDB; ADO41945.
XX PT Composition useful for treating cancer, viral infection, bacterial
XX PT infection, parasitic infection, inflammatory conditions, comprises
XX PT construct having complement receptor 2 and modulator of complement
XX PT activity.
XX PS Example 4; SEQ ID NO 4; 184pp; English.
XX CC This invention relates to novel targeted modulators of the complement
XX CC receptor 2 (CR2) protein that is involved in regulating complement
XX CC activity. Specifically, it refers to immunoconjugate compositions
XX CC comprising a construct that has a complement inhibitor linked to the CR2,
XX CC which can be used to modulate the complement system i.e. the series of blood
XX CC proteins that are major effectors of the immune system. The present
XX CC invention describes compositions that can be used to treat various
XX CC cancers including Hodgkin lymphoma, myeloid leukaemia and hypoxic
XX CC tumours, viral infections such as herpes simplex virus, cytomegalovirus
XX CC and Epstein-Barr virus, as well as inflammatory conditions for example
XX CC rheumatoid arthritis, Crohn's disease and systemic lupus erythematosus.
XX CC Accordingly, these compositions exhibit cytostatic, antiasthmatic,
XX CC antiinflammatory, dermatological, immunosuppressive, antiarthritic,
XX CC antihypertensive, vasotonic, antidiabetic, neuroprotective, anti-allergic,
XX CC anti-ulcer and antiviral activities. This polypeptide sequence is the
XX CC human complement inhibitor CD59 protein of the invention.
XX SQ Sequence 126 AA;
    Query Match 100.0%; Score 96; DB 8; Length 126;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FEHCNFDVTTTLRENE 17
Db 65 FEHCNFDVTTTLRENE 81
    |||||
RESULT 19
AAAY27311
XX ID AAY27311 standard; peptide; 127 AA.
XX AC AAY27311;
XX DT 05-NOV-1999 (first entry)
XX DE Human CD59 protein sequence.
XX KW CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic;
XX KW tumour therapy; complement-mediated inflammation; immune disorder;
XX KW immunovascularitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
XX KW plasma membrane antigen.
XX OS Homo sapiens.
XX PN W09940115-A2.
XX PD 12-AUG-1999.
XX PF 09-FEB-1999; 99WO-US002802.
XX PR 09-FEB-1998; 98US-00020393.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PA (BLOO-) BLOOD CENT RES FOUND INC.
XX PI Sims PJ;
XX DR WPI; 1999-527301/44.
XX CC Compounds modulating CD59 mediated complement activity, for treatment of,
XX PT e.g. immunovascularitis.
XX PS Disclosure; Fig 1A; 75pp; English.
XX CC The invention relates to compounds modulating CD59 mediated complement
XX CC activity. It provides (i) molecules structurally mimicking human CD59
XX CC amino acid residues 42-58 (region which serves as binding site for C5b-9
XX CC C9 interactions) when they are in a spatial orientation which can inhibit
XX CC the formation of the human C5b-9 complex. These mimetics specifically
XX CC bind to amino acid residues 359-384 of human C9. (ii) molecules
XX CC structurally mimicking C9 amino acids 359-384 when they are in a spatial
XX CC orientation which can promote the formation of the C5b-9 complex.
XX CC Compounds that mimic CD59 can be used to increase CD59 inhibition of C5b-
XX CC 9 complex assembly. This is especially useful in patients in need of
XX CC suppression of complement-mediated inflammation, e.g. immune disorders
XX CC and diseases such as immunovascularitis, rheumatoid arthritis, scleroderma.
XX CC Compounds that mimic C9 can be used to promote C5b-9 complex assembly.
XX CC This is useful in patients in need of complement activation. The
XX CC composition can be administered as an adjunct to tumour therapy. The
XX CC present sequence represents a human CD59 (a plasma membrane antigen)
XX CC protein sequence
XX SQ Sequence 127 AA;
    Query Match 100.0%; Score 96; DB 2; Length 127;
    Best Local Similarity 100.0%; Pred. No. 3.6e-07;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FEHCNFDVTTTLRENE 17
Db 66 FEHCNFDVTTTLRENE 82
    |||||
RESULT 20
AAAR04704
XX ID AAR04704 standard; protein; 128 AA.
XX AC AAR04704;
XX DT 25-MAR-2003 (revised)
XX DT 30-AUG-1990 (first entry)
XX DE Sequence of the 1F5 antigen derived from human cell membrane.
XX KW Human 1F5 antigen; immunodiagnosis; pernicious anaemia;
XX KW rheumatoid arthritis; systemic lupus erythematosus; glomerular nephritis.
XX OS Homo sapiens.
XX PN EP351313-A.
XX PD 17-JAN-1990.
XX PF 11-JUL-1989; 89EP-00401996.
XX PR 11-JUL-1988; 88JP-00172187.
XX PR 23-MAY-1989; 89JP-00129944.
XX PA (MITU) MITSUBISHI KASEI CORP.
XX PD
```

PI Okada H, Okada N, Nagami Y, Takahashi K, Takizawa H, Kondo J;
 XX WPI; 1990-016630/03
 DR N-PSDB; AAQ03116, AAN93318.
 XX New glyco:protein IF5 antigen - derived from human cell membrane,
 PT inhibits complement-mediated cell membrane damage.
 XX
 PS Claim 3; p. 11; 26pp; English.
 XX
 CC Typically it is prep'd. from human erythrocytes which are centrifuged and
 CC the cell membrane fraction suspended overnight in buffer contg. 1% n-
 CC octyl-beta-D-glucopyranoside (NOG). After centrifugation, the super-
 CC natant is treated with solid (NH4)2SO4 to 60% satn. After centrifugation
 CC the ppte. is dissolved in buffer contg. 0.1%NOG, then dialysed overnight
 CC against the same plus 0.15 M NaCl. IF5 antigen is a glycoprotein with a
 CC mol. wt. of 20-25 KD. It contains N-glycoside type carbohydrate chain and
 CC phosphatidylinositol. It inhibits complement-mediated cell membrane
 CC damage. It may be used to generate polyclonal or monoclonal antibodies
 CC (Abs) which may be used to determine the presence of IF5 antigen on the
 CC surface of erythrocytes, lymphocytes or other cells, thus enabling the
 CC diagnosis of diseases, such as pernicious anaemia, rheumatoid arthritis,
 CC systemic lupus erythematosus and glomerular nephritis. It may be used to
 CC treat disorders in which complement activation is involved. Abs to it may
 CC be used in targeting therapy, such as cancer cell lysis, or elimination
 CC of malignant cells. Residues 27-70 are encoded by a cDNA fragment of the
 CC gene which encodes IF5 antigen prep'd. by the polymerase chain reaction
 CC (in AAN93318). (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. NO. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDNDVTRLRENE 17
 |||||
 DB 67 FEHCNFDNDVTRLRENE 83

RESULT 21
 AAR07444
 ID AAR07444 standard; protein; 128 AA.
 XX
 AC AAR07444;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1991 (first entry)
 DE Human membrane attack complex inhibition factor (MACIF) gene product.
 XX
 XX Haemolysis; late complement components.
 KW
 XX Homo sapiens.
 OS

Key Location/Qualifiers
 FT Protein 26..128
 FT /label= Mature MACIF protein.
 XX
 PN EP394035-A.
 XX

PD 24-OCT-1990.
 XX
 XX 19-APR-1990; 90EP-00304203.
 XX
 PR 21-APR-1989; 89JP-00103088.
 PR 12-JUL-1989; 89JP-00179933.
 PR 06-SEP-1989; 89JP-00230983.
 PR 13-SEP-1989; 89JP-00238246.
 PR 21-SEP-1989; 89JP-00247818.
 PR 27-OCT-1989; 89JP-00281197.
 XX
 PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX Tomita M, Sugita Y, Takemoto T, Furuichi K, Takayama M;
 PI Yusakawa K, Yano S, Yamaji N;
 XX WPI; 1990-322496/43.
 DR N-PSDB; AAQ06262.
 XX
 PT Genes encoding protein with human MACIF activity - also expression
 PT vectors and proteins produced from expression of the genes.
 XX
 XX Disclosure; Fig 1; 49pp; English.
 XX
 CC Gene product may be expressed in large quantities and pure form from CHO
 CC cells, useful for inhibiting the activity of late complement components
 CC ie. haemolysis resulting from MAC formation. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. NO. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDNDVTRLRENE 17
 |||||
 DB 67 FEHCNFDNDVTRLRENE 83

RESULT 22
 AAR11876
 ID AAR11876 standard; protein; 128 AA.
 XX
 AC AAR11876;
 XX
 XX 24-JUL-1991 (first entry)
 DT
 XX Human lymphocyte surface antigen precursor.
 DE
 XX Ly-6; cancer; autoimmune disease; pre A precursor.
 KW
 XX Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Pre A precursor
 FT Protein 26..128
 FT /label= Mature surface antigen
 XX
 PN JP03081297-A.
 XX

PD 05-APR-1991.
 XX
 XX 23-AUG-1989; 89JP-00218183.
 XX
 XX 23-AUG-1989; 89JP-00218183.
 XX
 XX (TORA) TORAY IND INC.
 XX
 XX WPI; 1991-144848/20.
 DR N-PSDB; AAQ11684, AAQ11685, AAQ11686.
 XX

XX Surface antigen of human lymphocyte - and gene and antibody useful for
 PT investigation and treatment of autoimmune disease, cancer, infection,
 PT etc.
 XX
 XX Claim 5; Page 1203; 16pp; Japanese.

PS Clone is derived from the Ly-6 cDNA sequence from a human lymphocyte cDNA
 XX library. The product may be useful in the study and development of drugs
 CC for the treatment of autoimmune diseases and cancer. Probes may also be
 CC developed for the isolation of other gene families
 XX
 XX Sequence 128 AA;

Query Match 100.0%; Score 96; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | |
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 23
AAR80240
ID AAR80240 standard; protein; 128 AA.
XX AC AAR80240;
XX DT 25-MAR-2003 (revised)
XX DT 17-APR-1996 (first entry)
XX DE Human membrane attack complex inhibition factor.
XX DE
XX KW MACIF; membrane attack complex inhibition factor; complement system;
KW regulation; activation; final stage; inhibit damage; disease therapy;
KW type II allergy; type III allergy; inflammatory disease treatment;
KW phosphatidylinositol anchor; glycoprotein; diagnosis.
XX OS Homo sapiens.
XX FH
XX FT Key Location/Qualifiers
FT Peptide 1. .25
FT /label= secretory_signal_sequence
FT Protein 26. .128
FT /note= "human MACIF"
FT Binding-site 96. .128
FT /label= PI_anchor_attachment_signal_sequence
XX EP672683-A1.
XX
XX 20-SEP-1995.
XX
XX 19-APR-1990; 95EP-00200379.
XX
XX 21-APR-1989; 89JP-00103088.
XX 12-JUL-1989; 89JP-00179933.
XX 06-SEP-1989; 89JP-00230983.
XX 13-SEP-1989; 89JP-00238246.
XX 21-SEP-1989; 89JP-00247818.
XX 27-OCT-1989; 89JP-00281197.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX Tomita M, Sugita Y, Takemoto T, Furuichi K, Takayama M;
PI Kasukawa K, Yano S, Yamaji N, Ito K;
XX WPI; 1995-321975/42.
DR N-PSDB; AAQ98532.
XX
XX Peptide with human membrane attack complex inhibition factor activity -
PT also DNA and expression vectors used to regulate the complement system in
PT the final stage of complement activation.
XX
XX Disclosure; Fig 2; 49pp; English.
XX
XX Human membrane attack complex inhibition factor (MACIF) regulates the
CC complement system in the final stage of complement activation and
CC inhibits damage of human cells and tissues as a result of MAC formation.
CC Naturally occurring human MACIF is a glycoprotein of mol. wt. 18 +/- 1 kDa
CC (by SDS-PAGE) with a phosphatidylinositol (PI) anchor at position 76
CC (Glu) at the C-terminus. When the gene encoding MACIF is expressed in
CC bacteria, the gene (see AAQ98532) gives a modified human MACIF protein
CC comprising 128 amino acid residues (AAR80240); the PI anchor attachment
CC does not occur in that case. (Updated on 25-MAR-2003 to correct PF
CC field.)

XX SQ Sequence 128 AA;
Query Match 100.0%; Score 96; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | |
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 24
AAR86315
ID AAR86315 standard; protein; 128 AA.
XX AC AAR86315;
XX DT 11-MAR-1996 (first entry)
XX DE Human CD59.
XX DE
XX KW Terminal complement inhibitor protein; terminal CIP; CD59; CD46;
KW transmembrane terminal CIP; TWTCIP; Ly6 antigen; transgenic animal;
KW organ transplantation; glycosyl-phosphatidylinositol; GPI.
XX OS Homo sapiens.
XX FH
XX FT Key Location/Qualifiers
FT Peptide 1. .25
FT /label= sig_peptide
FT Region 28. .96
FT /label= Ly6 motif
FT Region 103. .128
FT /label= GPI anchor region
FT /note= "GPI anchor region corresponds to amino acids 78-
FT 103 of the mature CD59 protein"
XX WO9523512-A1.
XX
XX 08-SEP-1995.
XX
XX 01-MAR-1995; 95WO-US002944.
XX
XX 03-MAR-1994; 94US-00205720.
XX (ALEX-) ALEXION PHARM INC.
XX
XX Rother RP, Rollins S, Squinto SP;
PI WPI; 1995-320335/41.
XX N-PSDB; AAT03338.
XX
XX Terminal complement inhibitor chimeric protein and nucleic acid - esp.
PT against human complement, useful for protecting cells from complement
PT attack e.g. in organ transplantation.
XX
XX Disclosure; Page 63-64; 85pp; English.
XX
XX Human CD59 (AAR86315) is a terminal complement inhibitor protein (CIP)
CC that includes a C-terminal region involved in directing attachment of a
CC glycosyl-phosphatidylinositol (GPI) anchor. A chimeric transmembrane
CC terminal CIP (TWTCIP) comprising amino acids 1-77 of mature CD59 (i.e.
CC lacking the GPI anchor region) and the transmembrane domain (amino acids
CC 270-350) of human CD46, a membrane cofactor protein. The TWTCIP has been
CC expressed on the cell surfaces of the organs of transgenic animals. Such
CC transgenic organs are protected from human complement attack upon
CC transplantation
XX
XX SQ Sequence 128 AA;
Query Match 100.0%; Score 96; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;

KW	Immunosuppressive; cellular immune response; humoral immune response;
KW	Cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
KW	transplant rejection; human.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..25
FT	/note= "Signal peptide"
FT	Protein 26..128
FT	/note= "Mature CD59"
XX	
PN	US2003086940-A1.
XX	
PD	08-MAY-2003.
XX	
XX	
PF	20-AUG-2002; 2002US-00225519.
XX	
PR	10-AUG-2001; 2001US-00928267.
XX	(COST/) COSTA C.
PA	(PIZZ/) PIZZOLATO M.
PA	(FODO/) FODOR W.
XX	
PI	Costa C, Pizzolato M, Fodor W;
XX	WPI: 2003-625623/59.
DR	N-PSDB; ADA50040.
XX	
PT	New chimeric proteins comprising a first domain and a second domain
PT	capable of inhibiting a cellular and humoral immune response,
PT	respectively, useful for regulating humoral and cellular effector
PT	functions of the immune system.
XX	
PS	Disclosure; Page 28; 59pp; English.
XX	
CC	The invention relates to a chimaeric protein comprising a first domain
CC	capable of inhibiting a cellular immune response and a second domain
CC	capable of inhibiting a humoral immune response. Also included are a
CC	chimeric DNA construct (comprising a DNA sequence encoding a domain
CC	capable of inhibiting a cellular immune response and a DNA sequence
CC	encoding a domain capable of inhibiting a humoral immune response), a
CC	cloning vector comprising the DNA construct, a host cell transformed by
CC	the vector, a transgenic cell, tissue, organ or mammal comprising the
CC	chimeric protein, producing a mammal, mammalian organ, tissue or cells,
CC	where the mammal is useful as an organ donor for a human or organ, tissue
CC	or cells transplant into a human, by inserting a nucleic acid encoding a
CC	chimeric protein defined above into the mammal, organ, tissue or cells,
CC	where the protein is expressed in the mammal, organ, tissue or cells,
CC	defined regions of the DNA appearing as ADA50036 which encodes the pig
CC	CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
CC	regions of the CTLA4 protein ADA50037. The chimeric protein is useful in
CC	the protection of the porcine cell after xenotransplantation into a
CC	human, and in inhibiting humoral and cellular defence mechanism.
CC	Chimeras were produced comprising pig CTLA4 (cellular immune response
CC	region) and human CD59 (humoral response region), and of CTLA4 and human
CC	DAF (not defined). The present sequence represents human CD59.
XX	
SQ	Sequence 128 AA;
	Query Match 100.0%; Score 96; DB 7; Length 128;
	Best Local Similarity 100.0%; Pred. No. 3.6e-07;
	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FEHCNFNDVTRLRENE 17
Db	67 FEHCNFNDVTRLRENE 83
RESULT 28	
ADD25548	ID
ID	ADD225548 standard; protein; 128 AA.
XX	

AC	AD225548;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Binding domain-immunoglobulin fusion protein-associated protein #51.
XX	
KW	Binding domain; immunoglobulin; fusion protein; cytostatic;
KW	antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW	neuroprotective; hinge region; immunoglobulin heavy chain;
KW	CH2 constant region; CH3 constant region; IgG1;
KW	antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW	malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW	rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW	type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX	
OS	Unidentified.
XX	
PN	US2003118592-A1.
XX	
PD	26-JUN-2003.
XX	
XX	
PF	25-JUL-2002; 2002US-00207655.
XX	
PR	17-JAN-2001; 2001US-0367358P.
PR	17-JAN-2002; 2002US-00053530.
PR	03-JUN-2002; 2002US-0385691P.
XX	
PA	(GENE-) GENE-CRAFT INC.
XX	
PI	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX	WPI: 2003-801317/75.
DR	
XX	
PT	New binding domain-immunoglobulin fusion protein, useful for treating a
PT	subject having or suspected of having a malignant condition or a B-cell
PT	disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX	
XX	Disclosure; SEQ ID NO 109; 157pp; English.
XX	
CC	The invention relates to a binding domain-immunoglobulin fusion protein
CC	comprising a binding domain polypeptide that is fused to an
CC	immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC	CH2 constant region polypeptide that is fused to the hinge region
CC	polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC	polypeptide that is fused to the CH2 constant region polypeptide. The
CC	hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin
CC	hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC	region polypeptide, derived from (a) having 3 or more cysteine residues;
CC	where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC	contains 2 cysteine residues, where the first cysteine is not mutated; a
CC	mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC	(a) having 3 or more cysteine residues, where the mutated human IgG1
CC	immunoglobulin hinge region polypeptide contains no more than one
CC	cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC	polypeptide, derived from (a) having 3 or more cysteine residues; where
CC	the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC	no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC	capable of at least one immunological activity comprising antibody
CC	dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC	binding domain polypeptide is capable of specifically binding to an
CC	antigen. Also included are an isolated polynucleotide encoding the
CC	binding domain-immunoglobulin fusion protein, a recombinant expression
CC	construct comprising the polynucleotide (operably linked to a promoter),
CC	a host cell transformed or transfected with a recombinant expression
CC	construct, producing the binding domain-immunoglobulin fusion protein, a
CC	pharmaceutical composition comprising the binding domain-immunoglobulin
CC	fusion protein or polynucleotide and a carrier, and treating a subject
CC	having or suspected of having a malignant condition or a B-cell disorder.
CC	The binding domain-immunoglobulin fusion protein is useful for treating a
CC	subject having or suspected of having a malignant condition or a B-cell
CC	disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC	myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC	sclerosis or autoimmune disease. The present sequence is a binding domain

CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
Db 67 FEHCNFNDVTTTLRENE 83
|||||

RESULT 29
ADE58894
ID ADE58894 standard; protein; 128 AA.
XX
AC ADE58894;
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_000602, SEQ ID NO 4782.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX
PN WO2003016475-A2.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_000602.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
Db 67 FEHCNFNDVTTTLRENE 83
|||||

RESULT 30
ADD45530
ID ADD45530 standard; protein; 128 AA.
XX
AC ADD45530;
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_000602, SEQ ID NO 11194.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX
PN WO2003016475-A2.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_000602.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTRENE 17
 |||||
 Db 67 FEHCNFDVTTRENE 83

RESULT 31
 ADE58890
 ID ADE58890 standard; protein; 128 AA.
 AC ADE58890;
 XX
 DT 29-JAN-2004 (first entry)
 DE Human Protein NP_000602, SEQ ID NO 4778.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX WO2003016475-A2.
 PN
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 PR
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 PR
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; NP_000602.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTRENE 17
 |||||
 Db 67 FEHCNFDVTTRENE 83

RESULT 32
 ADJ69312
 ID ADJ69312 standard; protein; 128 AA.
 AC ADJ69312;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human heat mitochondrial protein as a therapeutic target SeqID1118.
 XX
 DE
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX WO2003087768-A2.
 PN
 XX 23-OCT-2003.
 XX
 XX 04-APR-2003; 2003WO-US010870.
 PF
 XX 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-038987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 DR
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT

PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1118; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteoparathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTTLRENE 17
|||||
Db 67 FEHCNFDVTTTLRENE 83

RESULT 33
ADL91008
ID ADL91008 standard; protein; 128 AA.
XX
XX AC ADL91008;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human CD59.
XX
XX KW gene; human; CD59; immune response inhibitor; xenotransplant rejection;
XX KW transgenic; organ donor.
XX
XX OS Homo sapiens.

XX
XX PN US2003157705-A1.
XX
XX PD 21-AUG-2003.

XX
XX PF 10-AUG-2001; 2001US-00928267.
XX
XX PR 10-AUG-2001; 2001US-00928267.

XX
XX PA (FODO/) FODOR W L.
XX
XX PA (PIZZ/) PIZZOLATO M.

XX
XX PI Fodor WL, Pizzolato M;

XX
XX WPI; 2003-766179/72.
XX
XX DR N-PSDB; ADL91007.

XX
XX PT New chimeric protein capable of inhibiting both cellular and humoral
XX PT immune responses, and DNA constructs encoding the chimeric protein,
XX PT useful for preventing and/or treating rejection of xenotransplants.

XX
XX PS Disclosure; Fig 2E2; 38pp; English.

XX
XX CC The invention relates to a chimeric protein capable of inhibiting both
XX CC cellular and humoral immune responses. The protein and DNA molecules are
XX CC useful in the prevention or treatment of humoral and cellular rejection
XX CC of xenotransplants. In particular, the DNAs may be used to produce

CC transgenic animals for use as tissue/organ donors, the cells of which are
CC protected from human cellular immune responses due to their expression of
CC the chimeric protein. The present sequence represents the amino acid
XX sequence of human CD59.

XX SQ Sequence 128 AA;

Query Match 100.0%; Score 96; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTTLRENE 17
|||||
Db 67 FEHCNFDVTTTLRENE 83

RESULT 34

ADN95931

ID ADN95931 standard; protein; 128 AA.

XX
XX AC ADN95931;

XX
XX DT 01-JUL-2004 (first entry)

XX
XX DE Human BEC/LSC-related protein sequence SeqID855.

XX
XX KW growth; differentiation; blood endothelial cell; BEC;
XX KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
XX KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cyostatic;
XX KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
XX KW inflammatory disease; cancer metastasis; lymphatic system; human.

XX
XX OS Homo sapiens.

XX
XX PN WC2003080640-A1.

XX
XX PD 02-OCT-2003.

XX
XX PF 07-MAR-2003; 2003WO-US006900.

XX
XX PR 07-MAR-2002; 2002US-0363019P.

XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA LTD.

XX
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

XX
XX WPI; 2003-876899/81.
XX
XX DR N-PSDB; ADN95932.

XX
XX PS Example 1; SEQ ID NO 855; 176pp; English.

XX
XX CC This invention relates to a method of differentially modulating the
XX CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX CC endothelial cells (LEC) comprises contacting endothelial cells with a
XX CC composition comprising an agent that differentially modulates blood or
XX CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX CC identifying a human subject with lymphoedema and with a mutation in at
XX CC least one allele of a gene encoding a LEC protein, where the mutation
XX CC correlates with lymphoedema in human subjects, and with the proviso that
XX CC the LEC protein is not VEGFR-3; and administering to the subject a
XX CC composition comprising a lymphatic growth agent selected from VEGF-C or
XX CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX CC the development of compounds with an antiangiogenic, cyostatic,
XX CC vasotropic or antiinflammatory activity or for gene therapy. The method
XX CC is useful in modulating the growth or differentiation of blood
XX CC endothelial cells or lymphatic endothelial cells, in treating hereditary
XX CC lymphoedema, in screening for an endothelial cell disorder or
XX CC predisposition to the disorder or in monitoring the efficacy or toxicity
XX CC of a drug on endothelial cells. The agent is useful in manufacturing a
XX CC medicament for the differential modulation of blood vessel endothelial
XX CC cell or lymphatic vessel endothelial cell growth or differentiation. The
XX CC lymphatic growth agent may also be used in manufacturing a medicament for

CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed protein which is related to the method of the invention. Note:
 CC This sequence does not appear in the specification but was obtained by
 CC the indexer using the source data given in table 14 of the specification.
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 96; DB 7; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFNDVTTTLRENE 17
 Db 67 FEHCNFNDVTTTLRENE 83
 |||||
 RESULT 35
 ADP23084
 ID ADP23084 standard; protein; 128 AA.
 XX
 AC ADP23084;
 XX
 DT 18-NOV-2004 (first entry)
 DE PRO polypeptide SEQ ID NO:178.
 XX
 KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipeoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 FN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX
 DR WPI; 2004-419628/39.
 DR N-PSDB; ADP23083.
 XX
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 178; 2940pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipeoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC

CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 96; DB 8; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFNDVTTTLRENE 17
 Db 67 FEHCNFNDVTTTLRENE 83
 |||||
 RESULT 36
 ABM83101
 ID ABM83101 standard; protein; 130 AA.
 XX
 AC ABM83101;
 XX
 DT 18-NOV-2004 (first entry)
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3350.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney BM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve JL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN41753.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 96; DB 8; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDNDVTTLRENE 17
 |||||
 Db 67 FEHCNFDNDVTTLRENE 83

RESULT 37

ID ADE07977 standard; protein; 190 AA.
 XX ADE07977;

DT 29-JAN-2004 (first entry)

DE Novel protein (useful for identifying genetic disorders) #132.

KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.

OS Unidentified.

XX WO2003054152-A2.

PN 03-JUL-2003.

PD 10-DEC-2002; 2002WO-US039555.

PF 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 12-APR-2002; 2002US-0372381P.

PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.

PR 24-APR-2002; 2002US-0376045P.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

XX WPI; 2003-569235/53.

DR N-PSDB; ADE07066.

XX New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1043; 1177pp; English.

PS The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels, as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.

XX SQ Sequence 190 AA;

Query Match 100.0%; Score 96; DB 7; Length 190;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDNDVTTLRENE 17
 |||||
 Db 129 FEHCNFDNDVTTLRENE 145

RESULT 38

AAU00685
 ID AAU00685 standard; protein; 260 AA.

XX AAU00685;

XX 07-SEP-2001 (first entry)

XX Human CTLA4-human CD59 chimeric protein.

XX CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity;
 KW C3 inhibitory activity; cellular immune response; xenotransplantation;
 KW humoral immune response; human serum complement; rodent; mouse; rabbit;
 KW rat; lagomorph; hare; ungulate; goat; sheep; mutant; mutein.

XX Homo sapiens.

XX Synthetic.

PN WO200130966-A2.

XX 03-MAY-2001.

XX 21-OCT-2000; 2000WO-US029151.

XX 22-OCT-1999; 99US-0161186P.

XX (ALEX-) ALEXION PHARM INC.

XX Fodor WL, Pizzolato M;

XX WPI; 2001-300497/31.

XX N-PSDB; AAS00679.

XX Chimeric protein useful for protecting xenotransplanted tissues by
 PT inhibiting cellular both humoral and immune responses, comprises a C5b-9
 PT and/or C3 inhibitory domain, and a T-cell inhibitory domain.

XX Example 1; Fig 2B(2); 51pp; English.

XX The sequence represents a CTLA4-CD59 chimeric protein, formed from human
 CC CTLA4 protein and human CD59 protein. Chimeric proteins comprising a
 CC domain having C5b-9 and/or C3 inhibitory activity (e.g. CTLA4) and a
 CC inhibiting both cellular immune responses and humoral immune responses.
 CC These polypeptides and their associated nucleic acids are useful for
 CC protecting pig cells of tissues and organs from both humoral and cellular
 CC rejection after xenotransplantation into humans. The sequences are
 CC capable of conferring resistance to humoral and cellular mechanisms of
 CC immune attack, to protect against human serum complement and to inhibit T
 CC cell activation. Transgenic animals (for example, rodents, e.g. mouse,
 CC rat; lagomorphs, e.g. rabbit, hare; and ungulates, e.g. pig, goat, sheep)
 CC expressing such a chimeric protein on the surfaces of their cells would
 CC have a higher chance of survival

XX SQ Sequence 260 AA;

Query Match 100.0%; Score 96; DB 4; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
 |||||
 Db 199 FEHCNFDVTVTLRENE 215

RESULT 39
 ADA50035
 ID ADA50035 standard; protein; 260 AA.
 XX
 AC ADA50035;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Pig CTLA4/human CD59 chimaeric protein #2.
 XX
 KW Immunosuppressive; cellular immune response; humoral immune response;
 KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
 KW transplant rejection; human; pig.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Homo sapiens.
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /note= "Human CD59 leader peptide"
 FT Protein 26..151
 FT /note= "Pig CTLA4"
 FT Peptide 152..157
 FT /note= "Synthetic (Asn-Ser)3 linker"
 FT Protein 158..260
 FT /note= "Human CD59"
 XX
 PN US2003086940-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 20-AUG-2002; 2002US-00225519.
 XX
 XX 10-AUG-2001; 2001US-00928267.
 XX
 XX (COST/) COSTA C.
 XX (PIZZ/) PIZZOLATO M.
 XX (FODO/) FODOR W.
 XX
 XX Costa C, Pizzolato M, Fodor W;
 XX WPI; 2003-625623/59.
 XX
 XX New chimeric proteins comprising a first domain and a second domain
 XX capable of inhibiting a cellular and humoral immune response,
 XX respectively, useful for regulating humoral and cellular effector
 XX functions of the immune system.
 XX
 XX Disclosure; Page 23-24; 59pp; English.

CC The invention relates to a chimaeric protein comprising a first domain
 CC capable of inhibiting a cellular immune response and a second domain
 CC capable of inhibiting a humoral immune response. Also included are a
 CC chimaeric DNA construct (comprising a DNA sequence encoding a domain
 CC capable of inhibiting a cellular immune response and a DNA sequence
 CC encoding a domain capable of inhibiting a humoral immune response), a
 CC cloning vector comprising the DNA construct, a host cell transformed by
 CC the vector, a transgenic cell, tissue, organ or mammal comprising the
 CC chimaeric protein, producing a mammal, mammalian organ, tissue or cells,
 CC where the mammal is useful as an organ donor for a human or organ, tissue
 CC or cells transplant into a human, by inserting a nucleic acid encoding a
 CC chimaeric protein defined above into the mammal, organ, tissue or cells,
 CC where the protein is expressed in the mammal, organ, tissue or cells,
 CC defined regions of the DNA appearing as ADA50036 which encodes the pig

CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
 CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in
 CC the protection of the porcine cell after xenotransplantation into a
 CC human, and in inhibiting humoral and cellular immune response.
 CC Chimaeras were produced comprising pig CTLA4 (cellular immune response
 CC region) and human CD59 (humoral response region), and of CTLA4 and human
 CC DAF (not defined). The present sequence represents a CTLA4/CD59 chimaera
 CC of the invention.
 XX
 SQ Sequence 260 AA;
 Query Match 100.0%; Score 96; DB 7; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
 |||||
 Db 199 FEHCNFDVTVTLRENE 215

RESULT 40
 ADL91002
 ID ADL91002 standard; protein; 260 AA.
 XX
 AC ADL91002;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human CTLA4-CD59.
 XX
 KW CTLA4; human; CD59; immune response inhibitor; xenotransplant rejection;
 KW transgenic; tissue donor; organ donor.
 XX
 OS Homo sapiens.
 XX
 XX US2003157705-A1.
 XX
 XX 21-AUG-2003.
 XX
 XX 10-AUG-2001; 2001US-00928267.
 XX
 XX 10-AUG-2001; 2001US-00928267.
 XX
 XX (FODO/) FODOR W L.
 XX (PIZZ/) PIZZOLATO M.
 XX
 XX Fodor WL, Pizzolato M;
 XX WPI; 2003-766179/72.
 XX N-PSDB; ADL91001.
 XX
 XX New chimeric protein capable of inhibiting both cellular and humoral
 XX immune responses, and DNA constructs encoding the chimeric protein,
 XX useful for preventing and/or treating rejection of xenotransplants.
 XX
 XX Disclosure; Fig 2B2; 38pp; English.

CC The invention relates to a chimeric protein capable of inhibiting both
 CC cellular and humoral immune responses. The protein and DNA molecules are
 CC useful in the prevention or treatment of humoral and cellular rejection
 CC of xenotransplants. In particular, the DNAs may be used to produce
 CC transgenic animals for use as tissue/organ donors, the cells of which are
 CC protected from human cellular immune responses due to their expression of
 CC the chimeric protein. The present sequence represents the amino acid
 CC sequence of human CTLA4-CD59.
 XX
 SQ Sequence 260 AA;
 Query Match 100.0%; Score 96; DB 7; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17

Db		 199 FEHCNFDVTTLRENE 215
RESULT 41		
AAU00684		
ID	AAU00684 standard; protein; 261 AA.	
XX AC	AAU00684;	
XX XX		
DT DT	11-SEP-2003 (revised)	
DT DT	07-SEP-2001 (first entry)	
XX XX		
DE DE	Porcine CTLA4-human CD59 chimeric protein.	
XX XX		
KW KW	CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity;	
KW KW	C3 inhibitory activity; cellular immune response; xenotransplantation;	
KW KW	humoral immune response; human serum complement; rodent; mouse; rabbit;	
KW KW	rat; lagomorph; hare; ungulate; goat; sheep; mutant; mutein.	
XX OS	Homo sapiens.	
OS OS	Sus scrofa.	
OS OS	Chimeric.	
PX PN	WC200130966-A2.	
XX XX		
PD PD	03-MAY-2001.	
XX XX		
PF PF	21-OCT-2000; 2000WO-US029151.	
XX XX		
PR PR	22-OCT-1999; 99US-0161186P.	
PA PA	(ALEX-) ALEXION PHARM INC.	
PI PI	Fodor WL, Pizzolato M;	
DR DR	WPI; 2001-300497/31.	
XX PS	N-PSDB; AAS00678.	
XX XX		
PT PT	Chimeric protein useful for protecting xenotransplanted tissues by	
PT PT	inhibiting cellular both humoral and immune responses, comprises a C5b-9	
PT PT	and/or C3 inhibitory domain, and a T-cell inhibitory domain.	
XX PS	Example 3; Fig 2A(2); 51pp; English.	
XX CC	The sequence represents a CTLA4-CD59 chimeric protein, formed from	
CC CC	porcine CTLA4 protein and human CD59 protein. Chimeric proteins	
CC CC	comprising a domain having C5b-9 and/or C3 inhibitory activity (e.g.	
CC CC	CTLA4) and a domain having T-cell inhibitory activity (e.g. CD59) are	
CC CC	capable of inhibiting both cellular immune responses and humoral immune	
CC CC	responses. These polypeptides and their associated nucleic acids are	
CC CC	useful for protecting pig cells of tissues and organs from both humoral	
CC CC	and cellular rejection after xenotransplantation into humans. The	
CC CC	sequences are capable of conferring resistance to humoral and cellular	
CC CC	mechanisms of immune attack, to protect against human serum complement	
CC CC	and to inhibit T-cell activation. Transgenic animals (for example,	
CC CC	rodents, e.g. mouse, rat; lagomorphs, e.g. rabbit, hare; and ungulates,	
CC CC	e.g. pig, goat, sheep) expressing such a chimeric protein on the surfaces	
CC CC	of their cells would have a higher chance of survival. (Updated on 11-SEP	
XX XX	-2003 to standardise OS field)	
XX SQ	Sequence 261 AA;	
	Query Match 100.0%; Score 96; DB 4; Length 261;	
	Best Local Similarity 100.0%; Fred. No. 7.5e-07;	
	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FEHCNFDVTTLRENE 17 	
Db	200 FEHCNFDVTTLRENE 216 	
RESULT 42		

CC of the invention.

XX Sequence 261 AA;

Query Match 100.0%; Score 96; DB 7; Length 261;

Best Local Similarity 100.0%; Pred. No. 7.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17

|||||

Db 200 FEHCNFDVTTTLRENE 216

RESULT 43

ADL91000

ID ADL91000 standard; protein; 261 AA.

XX

AC ADL91000;

XX 20-MAY-2004 (first entry)

DE Pig CTLA4-human CD59 chimeric protein.

XX pig; CTLA4; human; CD59; immune response inhibitor;
KW xenotransplant rejection; transgenic; tissue donor; organ donor.

XX Sus scrofa.

OS Homo sapiens.

OS Chimeric.

XX US2003157705-A1.

PN

XX

XX

PD 21-AUG-2003.

XX 10-AUG-2001; 2001US-00928267.

XX 10-AUG-2001; 2001US-00928267.

PR (FODO/) FODOR W L.

PA (PIZZ/) PIZZOLATO M.

PA (PIZZ/) PIZZOLATO M.

XX Fodor WL, Pizzolato M;

XX WPI; 2003-766179/72.

DR N-PSDB; ADL90999.

XX

XX New chimeric protein capable of inhibiting both cellular and humoral
PT immune responses, and DNA constructs encoding the chimeric protein,
PT useful for preventing and/or treating rejection of xenotransplants.

XX Disclosure; Fig 2A2; 38pp; English.

XX The invention relates to a chimeric protein capable of inhibiting both
CC cellular and humoral immune responses. The protein and DNA molecules are
CC useful in the prevention or treatment of humoral and cellular rejection
CC of xenotransplants. In particular, the DNAs may be used to produce
CC transgenic animals for use as tissue/organ donors, the cells of which are
CC protected from human cellular immune responses due to their expression of
CC the chimeric protein. The present sequence represents the amino acid
CC sequence of a pig CTLA4-human CD59 chimeric protein.

XX Sequence 261 AA;

Query Match

Best Local Similarity 100.0%; Score 96; DB 7; Length 261;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17

|||||

Db 200 FEHCNFDVTTTLRENE 216

RESULT 44

ADA50056

ID ADA50056 standard; protein; 270 AA.

XX

AC ADA50056;

DT 20-NOV-2003 (first entry)

XX

DE Pig CTLA4/human CD59 chimeric protein #3.

XX

XX Immunosuppressive; cellular immune response; humoral immune response;
KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
KW transplant rejection; human; pig.

XX

OS Chimeric.

OS Synthetic.

OS Homo sapiens.

OS Sus scrofa.

XX

FH Key Location/Qualifiers

FT Peptide 1..37

FT Protein /note= "Pig CTLA4 leader peptide"

FT Peptide 37..124

FT Peptide /note= "Pig CTLA4"

FT Peptide 125..130

FT Protein /note= "Synthetic (Asn-Ser)3 linker"

FT Protein 131..270

FT Protein /note= "Human CD59"

XX

PN US2003086940-A1.

XX

PD 08-MAY-2003.

XX

PF 20-AUG-2002; 2002US-00225519.

XX

PR 10-AUG-2001; 2001US-00928267.

XX

PA (COST/) COSTA C.

PA (PIZZ/) PIZZOLATO M.

PA (FODO/) FODOR W.

XX

PI Costa C, Pizzolato M, Fodor W;

XX WPI; 2003-625623/59.

DR N-PSDB; ADA50055.

XX

XX New chimeric proteins comprising a first domain and a second domain
PT capable of inhibiting a cellular and humoral immune response.
PT respectively, useful for regulating humoral and cellular effector
PT functions of the immune system.

XX Disclosure; Page 32-33; 59pp; English.

XX The invention relates to a chimeric protein comprising a first domain
CC capable of inhibiting a cellular immune response and a second domain
CC capable of inhibiting a humoral immune response. Also included are a
CC chimeric DNA construct (comprising a DNA sequence encoding a domain
CC capable of inhibiting a cellular immune response and a DNA sequence
CC encoding a domain capable of inhibiting a humoral immune response), a
CC cloning vector comprising the DNA construct, a host cell transformed by
CC the vector, a transgenic cell, tissue, organ or mammal comprising the
CC chimeric protein, producing a mammal, mammalian organ, tissue or cells,
CC where the mammal is useful as an organ donor for a human or organ, tissue
CC or cells transplant into a human, by inserting a nucleic acid encoding a
CC chimeric protein defined above into the mammal, organ, tissue or cells,
CC where the protein is expressed in the mammal, organ, tissue or cells,
CC defined regions of the DNA appearing as ADA50036 which encodes the pig
CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
CC regions of the CTLA4 protein ADA50037. The chimeric protein is useful in
CC the protection of the porcine cell after xenotransplantation into a
CC human, and in inhibiting humoral and cellular defence mechanism.
CC Chimaeras were produced comprising pig CTLA4 (cellular immune response
CC region) and human CD59 (humoral response region), and of CTLA4 and human
CC DAF (not defined). The present sequence represents a CTLA4/CD59 chimaera

CC of the invention.
XX
SQ Sequence 270 AA;

Query Match 100.0%; Score 96; DB 7; Length 270;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTRLRENE 17
DB 209 FEHCNFNDVTRLRENE 225
|||||

RESULT 45
ADA50058
ID ADA50058 standard; protein; 271 AA.
XX
AC ADA50058;
XX
DT 20-NOV-2003 (first entry)
XX
DE Pig CTLA4/human CD59 chimaeric protein #4.
XX
KW Immunosuppressive; cellular immune response; humoral immune response;
KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
KW transplant rejection; human; pig.
XX
OS Chimeric.
OS Synthetic.
OS Homo sapiens.
OS Sus scrofa.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..37
FT /note= "Pig CTLA4 leader peptide"
FT Protein 37..125
FT /note= "Pig CTLA4"
FT Peptide 125..131
FT /note= "Synthetic (Gly)6 linker"
FT Protein 131..271
FT /note= "Human CD59"
XX
XX US2003086940-A1.
XX
PD 08-MAY-2003.
XX
XX 20-AUG-2002; 2002US-00225519.
XX
XX 10-AUG-2001; 2001US-00928267.
XX
XX (COST/) COSTA C.
XX (PIZZ/) PIZZOLATO M.
XX (FODOR/) FODOR W.
XX
XX Costa C, Pizzolatto M, Fodor W;
XX
XX WPI; 2003-625623/59.
XX N-PSDB; ADA50057.
XX
XX New chimeric proteins comprising a first domain and a second domain
XX capable of inhibiting a cellular and humoral immune response,
XX respectively, useful for regulating humoral and cellular effector
XX functions of the immune system.
XX
XX Disclosure; Page 35; 59pp; English.
XX
XX The invention relates to a chimaeric protein comprising a first domain
XX capable of inhibiting a cellular immune response and a second domain
XX capable of inhibiting a humoral immune response. Also included are a
XX chimaeric DNA construct (comprising a DNA sequence encoding a domain
XX capable of inhibiting a cellular immune response and a DNA sequence
XX encoding a domain capable of inhibiting a humoral immune response), a
XX cloning vector comprising the DNA construct, a host cell transformed by

CC the vector, a transgenic cell, tissue, organ or mammal comprising the
CC chimaeric protein, producing a mammal, mammalian organ, tissue or cells,
CC where the mammal is useful as an organ donor for a human or organ, tissue
CC or cells transplant into a human, by inserting a nucleic acid encoding a
CC chimaeric protein defined above into the mammal, organ, tissue or cells,
CC where the protein is expressed in the mammal, organ, tissue or cells,
CC defined regions of the DNA appearing as ADA50036 which encodes the pig
CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in
CC the protection of the porcine cell after xenotransplantation into a
CC human, and in inhibiting humoral and cellular defence mechanism.
CC Chimaeras were produced comprising pig CTLA4 (cellular immune response
CC region) and human CD59 (humoral response region), and of CTLA4 and human
CC DAP (not defined). The present sequence represents a CTLA4/CD59 chimaera
CC of the invention.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 96; DB 7; Length 271;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTRLRENE 17
DB 210 FEHCNFNDVTRLRENE 226
|||||

RESULT 46
ADA041954
ID ADA041954 standard; protein; 330 AA.
XX
AC ADA041954;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human CD59-CR2 fusion protein SeqID 12.
XX
KW human; CD59; complement inhibitor; gene; ds; complement receptor 2; CR2;
KW chimeric; immunoconjugate; cancer; Hodgkin's lymphoma; myeloid leukaemia;
KW hypoxic tumour; viral infection; inflammatory condition;
KW rheumatoid arthritis; Crohn's disease; systemic lupus erythematosus;
KW cytostatic; antiasthmatic; antiinflammatory; dermatological;
KW immunosuppressive; antiarthritic; antirheumatic; vasotropic;
KW antidiabetic; neuroprotective; antiallergic; antiulcer; antiviral;
KW complement system.
XX
XX Homo sapiens.
XX Chimeric.
XX
XX WO2004045520-A2.
XX
XX 03-JUN-2004.
XX
XX 13-NOV-2003; 2003WO-US036459.
XX
XX 15-NOV-2002; 2002US-0426676P.
XX
XX (MUSC-) MUSC FOUND RES DEV.
XX
XX Tomlinson S;
XX
XX WPI; 2004-420518/39.
XX N-PSDB; ADO41953.
XX
XX Composition useful for treating cancer, viral infection, bacterial
XX infection, parasitic infection, inflammatory conditions, comprises
XX construct having complement receptor 2 and modulator of complement
XX activity.
XX
XX Claim 9; SEQ ID NO 12; 184pp; English.
XX
XX This invention relates to novel targeted modulators of the complement
XX receptor 2 (CR2) protein that is involved in regulating complement

CC activity. Specifically, it refers to immunoconjugate compositions
 CC comprising a construct that has a complement inhibitor linked to the CR2,
 CC which can be used to modulate the complement system i.e. the series of blood
 CC proteins that are major effectors of the immune system. The present
 CC invention describes compositions that can be used to treat various
 CC cancers including Hodgkin lymphoma, myeloid leukaemia and hypoxic
 CC tumours, viral infections such as herpes simplex virus, cytomegalovirus
 CC and Epstein-Barr virus, as well as inflammatory conditions for example
 CC rheumatoid arthritis, Crohn's disease and systemic lupus erythematosus.
 CC Accordingly, these compositions exhibit cytostatic, antiasthmatic,
 CC antiinflammatory, dermatological, immunosuppressive, antiarthritic,
 CC antirheumatic, vasotropic, antidiabetic, neuroprotective, antiallergic,
 CC antiulcer and antiviral activities. This polypeptide sequence is the
 CC human CD59-CR2 fusion protein (CD59 is a complement inhibitor) of the
 CC invention.
 CC
 XX
 SQ Sequence 330 AA;
 Query Match 100.0%; Score 96; DB 8; Length 330;
 Best Local Similarity 100.0%; Pred. No. 9.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFNDVTTTLRENE 17
 |||||
 DB 42 FEHCNFNDVTTTLRENE 58
 |||||
 RESULT 47
 ADO41950
 ID ADO41950 standard; protein; 334 AA.
 XX ADO41950;
 DT 26-AUG-2004 (first entry)
 XX Human CR2-CD59 fusion protein SeqID 7.
 DE human; CD59; complement inhibitor; gene; ds; complement receptor 2; CR2;
 KW chimeric; immunoconjugate; cancer; Hodgkin's lymphoma; myeloid leukaemia;
 KW hypoxic tumour; viral infection; inflammatory condition;
 KW rheumatoid arthritis; Crohn's disease; systemic lupus erythematosus;
 KW cytostatic; antiasthmatic; antiinflammatory; dermatological;
 KW immunosuppressive; antiarthritic; antirheumatic; vasotropic;
 KW antidiabetic; neuroprotective; antiallergic; antiulcer; antiviral;
 KW complement system.
 XX Homo sapiens.
 OS Chimeric.
 XX WO2004045520-A2.
 FN 03-JUN-2004.
 XX 13-NOV-2003; 2003WO-US036459.
 XX 15-NOV-2002; 2002US-0426676P.
 XX (MUSC-) MUSC FOUND RES DEV.
 XX Tomlinson S;
 XX WPI; 2004-420518/39.
 DR N-PSDB; ADO41949.
 XX Composition useful for treating cancer, viral infection, bacterial
 PT infection, parasitic infection, inflammatory conditions, comprises
 PT construct having complement receptor 2 and modulator of complement
 PT activity.
 XX Claim 10; SEQ ID NO 8; 184pp; English.
 PS This invention relates to novel targeted modulators of the complement
 XX receptor 2 (CR2) protein that is involved in regulating complement

CC activity. Specifically, it refers to immunoconjugate compositions
 CC comprising a construct that has a complement inhibitor linked to the CR2,
 CC which can be used to modulate the complement system i.e. the series of blood
 CC proteins that are major effectors of the immune system. The present
 CC invention describes compositions that can be used to treat various
 CC cancers including Hodgkin lymphoma, myeloid leukaemia and hypoxic
 CC tumours, viral infections such as herpes simplex virus, cytomegalovirus
 CC and Epstein-Barr virus, as well as inflammatory conditions for example
 CC rheumatoid arthritis, Crohn's disease and systemic lupus erythematosus.
 CC Accordingly, these compositions exhibit cytostatic, antiasthmatic,
 CC antiinflammatory, dermatological, immunosuppressive, antiarthritic,
 CC antirheumatic, vasotropic, antidiabetic, neuroprotective, antiallergic,
 CC antiulcer and antiviral activities. This polypeptide sequence is the
 CC human CR2-CD59 fusion protein (CD59 is a complement inhibitor) of the
 CC invention.
 CC
 XX
 SQ Sequence 334 AA;
 Query Match 100.0%; Score 96; DB 8; Length 334;
 Best Local Similarity 100.0%; Pred. No. 9.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFNDVTTTLRENE 17
 |||||
 DB 299 FEHCNFNDVTTTLRENE 315
 |||||

Search completed: June 8, 2005, 12:16:51
 Job time : 160 secs

Result No.	Score	Query #			ID	Description
		Match	Length	DB		
1	96	100.0	23	17	US-10-870-342A-14	Sequence 14, Appl
2	96	100.0	26	17	US-10-870-342A-20	Sequence 20, Appl
3	96	100.0	30	17	US-10-870-342A-15	Sequence 15, Appl
4	96	100.0	42	17	US-10-870-342A-18	Sequence 18, Appl
5	96	100.0	70	15	US-10-332-047-3	Sequence 3, Appl
6	96	100.0	70	16	US-10-742-887-39	Sequence 39, Appl
7	96	100.0	71	15	US-10-332-047-6	Sequence 6, Appl
8	96	100.0	71	16	US-10-742-887-42	Sequence 42, Appl
9	96	100.0	77	14	US-10-403-340-3	Sequence 3, Appl
10	96	100.0	77	15	US-10-332-047-1	Sequence 1, Appl
11	96	100.0	77	16	US-10-742-887-37	Sequence 37, Appl

; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-20

Query Match 100.0%; Score 96; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 5 FEHCNFDVTTTLRENE 21

RESULT 3
US-10-870-342A-15
; Sequence 15, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-15

Query Match 100.0%; Score 96; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 12 FEHCNFDVTTTLRENE 28

RESULT 4
US-10-870-342A-18
; Sequence 18, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-18

Query Match 100.0%; Score 96; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 21 FEHCNFDVTTTLRENE 37

RESULT 5
US-10-332-047-3
; Sequence 3, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-332-047-3

Query Match 100.0%; Score 96; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 42 FEHCNFDVTTTLRENE 58

RESULT 6
US-10-742-887-39
; Sequence 39, Application US/10742887
; Publication No. US20040266684A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/10/742,887
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/09/612,314
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT634
US-10-742-887-39

Query Match 100.0%; Score 96; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17

```
Db          42 FEHCNFNDVTTTLRENE 58
|||||
RESULT 7
US-10-332-047-6
; Sequence 6, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR FILING DATE: 2003-01-06
; PRIOR FILING DATE: 2001-07-06
; PRIOR FILING DATE: 2001-07-06
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-332-047-6
Query Match          100.0%; Score 96; DB 15; Length 71;
Best Local Similarity 100.0%; Pred. No. 6.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 FEHCNFNDVTTTLRENE 17
|||||
Db          42 FEHCNFNDVTTTLRENE 58
|||||
RESULT 8
US-10-742-887-42
; Sequence 42, Application US/10742887
; Publication No. US20040266684A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/10/742,887
; CURRENT FILING DATE: 2003-12-23
; PRIOR FILING DATE: 2003-12-23
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: US/09/612,314
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2061
US-10-742-887-42
Query Match          100.0%; Score 96; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 6.9e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 FEHCNFNDVTTTLRENE 17
|||||
Db          42 FEHCNFNDVTTTLRENE 58
|||||
RESULT 9
US-10-403-340-3
; Sequence 3, Application US/10403340
; Publication No. US20030166565A1
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: Compositions and Methods to Inhibit the
; C5b-9 Complex of Complement
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/403,340
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,393B
; FILING DATE: 03-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-403-340-3
Query Match          100.0%; Score 96; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 7.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 FEHCNFNDVTTTLRENE 17
|||||
Db          42 FEHCNFNDVTTTLRENE 58
|||||
RESULT 10
US-10-332-047-1
; Sequence 1, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
```

; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS

; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332.047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-047-1

Query Match 100.0%; Score 96; DB 15; Length 77;
Best Local Similarity 100.0%; Pred. No. 7.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 11

US-10-742-887-37
; Sequence 37, Application US/10742887
; Publication No. US20040266684A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/10/742.887
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/09/612.314
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214.913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT631
US-10-742-887-37

Query Match 100.0%; Score 96; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 7.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 12

US-10-332-047-4
; Sequence 4, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH

; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS

; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332.047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-332-047-4

Query Match 100.0%; Score 96; DB 15; Length 82;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 13

US-10-742-887-40
; Sequence 40, Application US/10742887
; Publication No. US20040266684A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/10/742.887
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/09/612.314
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214.913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2060
US-10-742-887-40

Query Match 100.0%; Score 96; DB 16; Length 82;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 14

US-10-332-047-5
; Sequence 5, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:

; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-332-047-5

Query Match 100.0%; Score 96; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
DB 43 FEHCNFNDVTTTLRENE 59

RESULT 15
US-10-742-887-41
; Sequence 41, Application US/10742887
; Publication No. US2004026684A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/10/742,887
; CURRENT FILING DATE: 2003-12-23
; PRIOR FILING DATE: US/09/612,314
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT635
US-10-742-887-41

Query Match 100.0%; Score 96; DB 16; Length 83;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
DB 43 FEHCNFNDVTTTLRENE 59

RESULT 16
US-10-332-047-9

; Sequence 9, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-332-047-9

Query Match 100.0%; Score 96; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
DB 42 FEHCNFNDVTTTLRENE 58

RESULT 17
US-10-332-047-7
; Sequence 7, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-332-047-7

Query Match 100.0%; Score 96; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 9.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | |
DB 42 FEHCNFNDVTTTLRENE 58

RESULT 18
US-10-332-047-8
; Sequence 8, Application US/10332047

; Publication No. US20040043432A1
; GENERAL INFORMATION:
; APPLICANT: ROWLING, PAMELA JANE ELIZABETH
; APPLICANT: SMITH, GEOFFREY PAUL
; APPLICANT: RIDLEY, SIMON HUGH
; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-332-047-8

Query Match 100.0%; Score 96; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 43 FEHCNFDVTTTLRENE 59

RESULT 19
US-10-870-342A-6
; Sequence 6, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-6

Query Match 100.0%; Score 96; DB 17; Length 103;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 42 FEHCNFDVTTTLRENE 58

RESULT 20
US-10-870-342A-7
; Sequence 7, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7

; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: Lys is glycosylated
US-10-870-342A-7

Query Match 100.0%; Score 96; DB 17; Length 103;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 42 FEHCNFDVTTTLRENE 58

RESULT 21
US-10-870-342A-8
; Sequence 8, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Lys is glycosylated
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Lys is glycosylated
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: Lys is glycosylated
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65)..(66)
; OTHER INFORMATION: Lys is glycosylated
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85)..(85)
; OTHER INFORMATION: Lys is glycosylated
US-10-870-342A-8

Query Match 100.0%; Score 96; DB 17; Length 103;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 42 FEHCNFDVTTTLRENE 58

RESULT 22
US-10-883-576-12
; Sequence 12, Application US/10883576
; Publication No. US20050037400A1
; GENERAL INFORMATION:
; APPLICANT: Messier, Walter
; TITLE OF INVENTION: Methods to Identify Polynucleotide and Polypeptide Sequences
; TITLE OF INVENTION: Which may be Associated with Physiological and Medical Conditions

FILE REFERENCE: GENO200.2 CIP3
CURRENT APPLICATION NUMBER: US/10/883,576
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 10/098,600
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: US 60/545,604
PRIOR FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US 60/484,030
PRIOR FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 09/942,252
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 09/240,915
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/098,987
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: US 60/073,263
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 105
TYPE: PRT
ORGANISM: Pan troglodytes
US-10-883-576-12

Query Match 100.0%; Score 96; DB 17; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||

Db 43 FEHCNFDVTTTLRENE 59
|||||

RESULT 23
US-10-403-340-1
Sequence 1, Application US/10403340
Publication No. US20030166565A1
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
St.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 27-Mar-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR# 170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-403-340-1

Query Match 100.0%; Score 96; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||

Db 66 FEHCNFDVTTTLRENE 82
|||||

RESULT 24
US-09-928-267-25
Sequence 25, Application US/09928267
Publication No. US20030157705A1
GENERAL INFORMATION:
APPLICANT: William, Fodor
TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
FILE REFERENCE: 1087-19
CURRENT APPLICATION NUMBER: US/09/928,267
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 128
TYPE: PRT
ORGANISM: human
US-09-928-267-25

Query Match 100.0%; Score 96; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||

Db 67 FEHCNFDVTTTLRENE 83
|||||

RESULT 25
US-09-928-267-26
Sequence 26, Application US/09928267
Publication No. US20030157705A1
GENERAL INFORMATION:
APPLICANT: William, Fodor
TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
FILE REFERENCE: 1087-19
CURRENT APPLICATION NUMBER: US/09/928,267
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 128
TYPE: PRT
ORGANISM: human
US-09-928-267-26

Query Match 100.0%; Score 96; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||

```

; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1118
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1118

Query Match      100.0%; Score 96; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTTLRLENE 17
Db      67 FEHCNFNDVTTLRLENE 83

RESULT 29
US-10-759-181A-20
; Sequence 20, Application US/10759181A
; Publication No. US20040163140A1
; GENERAL INFORMATION:
; APPLICANT: MORGAN, BRYAN P.
; APPLICANT: RUSHMERE, NEIL K.
; APPLICANT: HINCHLIFFE, STEWART J.
; APPLICANT: VAN DEN BERG, CARMEN W.
; TITLE OF INVENTION: MODIFIED BIOLOGICAL MATERIAL
; FILE REFERENCE: WN/KH/JJ/WCM
; CURRENT APPLICATION NUMBER: US/10/759,181A
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: PCT/GB99/01085
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: GB 9807520.3
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-759-181A-20

Query Match      100.0%; Score 96; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTTLRLENE 17
Db      67 FEHCNFNDVTTLRLENE 83

RESULT 30
US-10-870-342A-5
; Sequence 5, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17

```

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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-5

Query Match          100.0%; Score 96; DB 17; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FEHCNFNDVTTTLRENE 17
Db      67 FEHCNFNDVTTTLRENE 83

RESULT 31
US-10-482-029-98
; Sequence 98, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-98

Query Match          100.0%; Score 96; DB 17; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FEHCNFNDVTTTLRENE 17
Db      67 FEHCNFNDVTTTLRENE 83
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; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 132
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-558-132

Query Match          100.0%; Score 96; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FEHCNFNDVTTTLRENE 17
Db      129 FEHCNFNDVTTTLRENE 145

RESULT 33
US-09-928-267-13
; Sequence 13, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Fodor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 260
; TYPE: PRT
; ORGANISM: human
US-09-928-267-13

Query Match          100.0%; Score 96; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FEHCNFNDVTTTLRENE 17
Db      199 FEHCNFNDVTTTLRENE 215

RESULT 34
US-09-928-267-14
; Sequence 14, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Fodor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 260
; TYPE: PRT
; ORGANISM: human
US-09-928-267-14

Query Match          100.0%; Score 96; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTRLRENE 17
|||||

Db 199 FEHCNFNDVTRLRENE 215

RESULT 35

US-10-225-519-4

; Sequence 4, Application US/10225519

; Publication No. US20030086940A1

; GENERAL INFORMATION:

; APPLICANT: Costa, Cristina

; APPLICANT: Pizzolato, Maryellen C.

; APPLICANT: Fodor, William L.

; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL

; FILE REFERENCE: 33-CIP

; CURRENT APPLICATION NUMBER: US/10/225,519

; CURRENT FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: US 09/928,267

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/29151

; PRIOR FILING DATE: 2000-10-21

; PRIOR APPLICATION NUMBER: US 60/161,186

; PRIOR FILING DATE: 1999-10-22

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: DNA used in the cloning of human CTLA4 - human CD59 chimeric mole

; OTHER INFORMATION: cules.

; NAME/KEY: misc_feature

; LOCATION: (37)..(111)

; OTHER INFORMATION: CD59 leader peptide region

; NAME/KEY: misc_feature

; LOCATION: (118)..(489)

; OTHER INFORMATION: CTLA4 coding region

; NAME/KEY: misc_feature

; LOCATION: (490)..(507)

; OTHER INFORMATION: (AS)3 linker region.

; NAME/KEY: misc_feature

; LOCATION: (508)..(616)

; OTHER INFORMATION: CD59 coding region

; US-10-225-519-4

Query Match

Best Local Similarity 100.0%; Score 96; DB 14; Length 260;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTRLRENE 17

|||||

Db 199 FEHCNFNDVTRLRENE 215

RESULT 36

US-09-928-267-9

; Sequence 9, Application US/09928267

; Publication No. US20030157705A1

; GENERAL INFORMATION:

; APPLICANT: William, Fodor

; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND

; FILE REFERENCE: 1087-19

; CURRENT APPLICATION NUMBER: US/09/928,267

; CURRENT FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 261

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: DNA used in the cloning of porcine CTLA4 - human CD59 chimeric mo

; OTHER INFORMATION: lecules.

; NAME/KEY: misc_feature

; LOCATION: (38)..(112)

; OTHER INFORMATION: CD59 leader peptide region

; NAME/KEY: misc_feature

; LOCATION: (119)..(493)
; OTHER INFORMATION: CTLA4 coding region
; NAME/KEY: misc feature
; LOCATION: (494)..(511)
; OTHER INFORMATION: (G) 6 linker region.
; NAME/KEY: misc feature
; LOCATION: (512)..(820)
; OTHER INFORMATION: CD59 coding region
US-10-225-519-2

Query Match 100.0%; Score 96; DB 14; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTRLRENE 17
| | | | | | | | | | | | | | | | | | | | | |
Db 200 FEHCNFNDVTRLRENE 216

RESULT 39
US-10-225-519-25
; Sequence 25, Application US/10225519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Pizzolato, Maryellen C.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric porcine CTLA4-human CD59 with porcine CTLA4 leader sequence
; NAME/KEY: misc feature
; LOCATION: (24)..(134)
; OTHER INFORMATION: Porcine CTLA4 leader sequence.
; NAME/KEY: misc feature
; LOCATION: (135)..(506)
; OTHER INFORMATION: Porcine CTLA4 coding region.
; NAME/KEY: misc feature
; LOCATION: (507)..(524)
; OTHER INFORMATION: (AS) 3 linker region.
; NAME/KEY: misc feature
; LOCATION: (525)..(833)
; OTHER INFORMATION: Human CD59 coding region.
US-10-225-519-25

Query Match 100.0%; Score 96; DB 14; Length 270;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTRLRENE 17
| | | | | | | | | | | | | | | | | | | | | |
Db 209 FEHCNFNDVTRLRENE 225

RESULT 40
US-10-225-519-27
; Sequence 27, Application US/10225519

; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa, Cristina
; APPLICANT: Pizzolato, Maryellen C.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric porcine CTLA4-human CD59 with porcine CTLA4 leader sequence
; NAME/KEY: misc feature
; LOCATION: (24)..(134)
; OTHER INFORMATION: Porcine CTLA4 leader sequence.
; NAME/KEY: misc feature
; LOCATION: (135)..(509)
; OTHER INFORMATION: Porcine CTLA4 coding sequence.
; NAME/KEY: misc feature
; LOCATION: (510)..(527)
; OTHER INFORMATION: (G) 6 linker region.
; NAME/KEY: misc feature
; LOCATION: (528)..(836)
; OTHER INFORMATION: Human CD59 coding region.
US-10-225-519-27

Query Match 100.0%; Score 96; DB 14; Length 271;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTRLRENE 17
| | | | | | | | | | | | | | | | | | | | | |
Db 210 FEHCNFNDVTRLRENE 226

Search completed: June 8, 2005, 11:55:33
Job time : 155 secs

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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:43:47 ; Search time 42 Seconds
(without alignments)
30.215 Million cell updates/sec

Title: US-09-020-393b-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	70	4	US-09-612-314A-39
2	96	100.0	71	4	US-09-612-314A-42
3	96	100.0	77	4	US-09-612-314A-37
4	96	100.0	82	4	US-09-612-314A-40
5	96	100.0	83	4	US-09-612-314A-41
6	96	100.0	103	1	US-08-271-562-1
7	96	100.0	103	1	US-08-087-007-3
8	96	100.0	103	2	US-08-696-777-1
9	96	100.0	103	3	US-08-483-433-3
10	96	100.0	103	5	PCT-US92-05920-3
11	96	100.0	105	3	US-09-591-435-12
12	96	100.0	115	4	US-09-513-999C-7845
13	96	100.0	115	4	US-09-513-999C-7846
14	96	100.0	115	4	US-09-513-999C-7847
15	96	100.0	128	6	5179198-1
16	96	100.0	128	6	5521296-1
17	96	100.0	128	6	5179198-1
18	96	100.0	128	6	5521296-1
19	96	100.0	135	4	US-09-949-016-9460
20	81	84.4	121	3	US-09-591-435-13
21	46	47.9	294	4	US-09-252-991A-29464
22	44	45.8	290	3	US-09-134-001C-4972
23	43	44.8	15	4	US-09-835-752-1
24	42	43.8	203	4	US-09-270-767-58029
25	42	43.8	215	4	US-09-248-796A-21597
26	42	43.8	404	4	US-09-248-796A-14911
27	42	43.8	415	4	US-09-248-796A-14912

28 42 43.8 533 4 US-09-270-767-42709 Sequence 42709, A
29 41 42.7 265 4 US-09-538-092-537 Sequence 537, App
30 41 42.7 410 4 US-09-543-681A-5407 Sequence 5407, Ap
31 41 42.7 1162 2 US-08-663-566A-15 Sequence 15, Appl
32 41 42.7 1162 2 US-08-023-610-15 Sequence 15, Appl
33 41 42.7 1162 2 US-08-288-065A-15 Sequence 15, Appl
34 41 42.7 1162 2 US-08-362-240A-15 Sequence 15, Appl
35 41 42.7 1162 5 PCT-US95-10245-15 Sequence 15, Appl
36 41 42.7 3433 4 US-09-091-501B-10 Sequence 10, Appl
37 41 42.7 3433 4 US-09-538-092-1136 Sequence 1136, Ap
38 40 41.7 61 4 US-09-489-039A-11913 Sequence 11913, A
39 40 41.7 174 4 US-09-270-767-32551 Sequence 32551, A
40 40 41.7 174 4 US-09-270-767-47768 Sequence 47768, A
41 40 41.7 217 1 US-08-277-231A-2 Sequence 2, Appli
42 40 41.7 217 1 US-08-277-231A-12 Sequence 12, Appl
43 40 41.7 217 2 US-08-473-750-1 Sequence 1, Appli
44 40 41.7 217 2 US-08-473-750-5 Sequence 5, Appli
45 40 41.7 217 2 US-08-477-326-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-612-314A-39
; Sequence 39, Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/09/612,314A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT634
US-09-612-314A-39

Query Match 100.0%; Score 96; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTRLRENE 17
| | | | | | | | | | | | | | | | | | | | | |
Db 42 FEHCNFDVTRLRENE 58

RESULT 2

US-09-612-314A-42
; Sequence 42, Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/09/612,314A

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; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2061
US-09-612-314A-42

Query Match          100.0%; Score 96; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
    |||||
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 3
US-09-612-314A-37
; Sequence 37, Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/09/612,314A
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT631
US-09-612-314A-37

Query Match          100.0%; Score 96; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
    |||||
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 4
US-09-612-314A-40
; Sequence 40, Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
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; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/09/612,314A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2060
US-09-612-314A-40

Query Match          100.0%; Score 96; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
    |||||
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 5
US-09-612-314A-41
; Sequence 41, Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAN
; APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
; TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
; FILE REFERENCE: 37945-0004
; CURRENT APPLICATION NUMBER: US/09/612,314A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/214,913
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/EP97/03715
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: GB 96 148 71.3
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT635
US-09-612-314A-41

Query Match          100.0%; Score 96; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 9.8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
    |||||
Db 43 FEHCNFNDVTTTLRENE 59

RESULT 6
US-08-271-562-1
; Sequence 1, Application US/08271562
; Patent No. 5573940
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
```

APPLICANT: Bothwell, Alfred L.M.
TITLE OF INVENTION: Genetic Inhibition of Complement
TITLE OF INVENTION: Mediated Inflammatory Response
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729926
FILING DATE: 15-JUL-1991
APPLICATION NUMBER: US 07/365199
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 112CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
CELL TYPE: Erythrocyte
US-08-271-562-1

Query Match 100.0%; Score 96; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTLRENE 17
|||||
Db 42 FEHCNFDVTVTLRENE 58

RESULT 7

US-08-087-007-3
Sequence 3, Application US/08087007
Patent No. 5705732 5684223
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
APPLICANT: Bothwell, Alfred L.M.
APPLICANT: Elliott, Eileen A.
APPLICANT: Flavell, Richard A.
APPLICANT: Madri, Joseph
APPLICANT: Rollins, Scott
APPLICANT: Bell, Leonard
APPLICANT: Squinto, Stephen
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,007
FILING DATE: 19930701
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD59
US-08-087-007-3

Query Match 100.0%; Score 96; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTLRENE 17
|||||
Db 42 FEHCNFDVTVTLRENE 58

RESULT 8

US-08-696-777-1
Sequence 1, Application US/08696777
Patent No. 5955441
GENERAL INFORMATION:
APPLICANT: Sims, Peter, J.
APPLICANT: Bothwell, Alfred, L. M.
TITLE OF INVENTION: Genetic Inhibition of Complement Mediated
TITLE OF INVENTION: Inflammatory Response
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,777
FILING DATE: 13-AUG-1996

/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF 112cipdiv
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-873-8794
/ TELEFAX: (404)-873-8795
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 103 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-696-777-1

Query Match 100.0%; Score 96; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
Db 42 FEHCNFDVTTTLRENE 58

RESULT 9
US-08-483-433-3
/ Sequence 3, Application US/08483433
/ Patent No. 6100443
/ GENERAL INFORMATION:
/ APPLICANT: Sims et al.
/ TITLE OF INVENTION: Universal Donor Cells
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: 2800 One Atlantic Center
/ STREET: 1201 West Peachtree Street
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: U.S.
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/483,433
/ FILING DATE:

/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/087,007
/ FILING DATE: July 1, 1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/906,394
/ FILING DATE: June 29, 1992
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF135cip2 div
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-873-8794
/ TELEFAX: 404-873-9794
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 103 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein

/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ IMMEDIATE SOURCE:
/ CLONE: CD59
US-08-483-433-3

Query Match 100.0%; Score 96; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
Db 42 FEHCNFDVTTTLRENE 58

RESULT 10
PCT-US92-05920-3
/ Sequence 3, Application PC/TUS9205920
/ GENERAL INFORMATION:
/ APPLICANT: Sims, Peter J.
/ APPLICANT: Bothwell, Alfred L.M.
/ APPLICANT: Elliott, Eileen A.
/ APPLICANT: Flavell, Richard A.
/ APPLICANT: Madri, Joseph
/ APPLICANT: Rollins, Scott
/ APPLICANT: Bell, Leonard
/ APPLICANT: Squinto, Stephen
/ TITLE OF INVENTION: Universal Donor Cells
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kilpatrick & Cody
/ STREET: 1100 Peachtree Street, Suite 2800
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: U.S.
/ ZIP: 30309-4530
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05920
/ FILING DATE: 19920714
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF135
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-815-6500
/ TELEFAX: 404-815-6555
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 103 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ IMMEDIATE SOURCE:
/ CLONE: CD59
PCT-US92-05920-3

Query Match 100.0%; Score 96; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 42 FEHCNFNDVTTTLRENE 58

RESULT 11
US-09-591-435-12
; Sequence 12, Application US/09591435
; Patent No. 6280953
; GENERAL INFORMATION:
; APPLICANT: MESSIER, WALTER
; APPLICANT: SIKELA, JAMES M
; TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
; TITLE OF INVENTION: AND MEDICAL CONDITIONS
; FILE REFERENCE: GENO.200.2
; CURRENT APPLICATION NUMBER: US/09/591,435
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/591,435
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/240,915
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,263
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/098,987
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-591-435-12

Query Match 100.0%; Score 96; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 43 FEHCNFNDVTTTLRENE 59

RESULT 12
US-09-513-999C-7845
; Sequence 7845, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7845
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 10.4
; OTHER INFORMATION: seq VLFGLLLVLAVFC/HS
US-09-513-999C-7845

Query Match 100.0%; Score 96; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 13
US-09-513-999C-7846
; Sequence 7846, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7846
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 10.4
; OTHER INFORMATION: seq VLFGLLLVLAVFC/HS
US-09-513-999C-7846

Query Match 100.0%; Score 96; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 14
US-09-513-999C-7847
; Sequence 7847, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7847
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 10.4
; OTHER INFORMATION: seq VLFGLLLVLAVFC/HS
US-09-513-999C-7847

Query Match 100.0%; Score 96; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 15

5179198-1

; Patent No. 5179198

; APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI;

; TAKASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN

; TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/376,828

; FILING DATE: 07-JUL-1989

; SEQ ID NO:1:

; LENGTH: 128

5179198-1

Query Match 100.0%; Score 96; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 16

5521296-1

; Patent No. 5521296

; APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI;

; TAKASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN

; TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR

; NUMBER OF SEQUENCES: 12

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/739,211

; FILING DATE: 01-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 376,828

; FILING DATE: 07-JUL-1989

; SEQ ID NO:1:

; LENGTH: 128

5521296-1

Query Match 100.0%; Score 96; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 17

5179198-1

; Patent No. 5179198

; APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI;

; TAKASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN

; TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/376,828

; FILING DATE: 07-JUL-1989

; SEQ ID NO:1:

; LENGTH: 128

5179198-1

Query Match 100.0%; Score 96; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 18

5521296-1

; Patent No. 5521296

; APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI;

; TAKASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN

; TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR

; NUMBER OF SEQUENCES: 12

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/739,211

; FILING DATE: 01-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 376,828

; FILING DATE: 07-JUL-1989

; SEQ ID NO:1:

; LENGTH: 128

5521296-1

Query Match 100.0%; Score 96; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 67 FEHCNFNDVTTTLRENE 83

RESULT 19

US-09-949-016-9460

; Sequence 9460, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9460

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-9460

Query Match 100.0%; Score 96; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTTLRENE 17
|||||
Db 74 FEHCNFNDVTTTLRENE 90

Search completed: June 8, 2005, 11:56:50
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 10:57:53 ; Search time 38 seconds
(without alignments)
43.044 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFDVTVTLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	29.2	15	2 A61612	allatostatin - tob
2	25	26.0	15	2 PC2215	fibrinogenolytic p
3	24	25.0	13	2 H56046	urinary tract ston
4	23	24.0	9	2 A11497	transaldolase (EC
5	23	24.0	14	2 PS0371	hypothetical prote
6	23	24.0	17	2 A61117	somatostatin precu
7	22	22.9	16	2 A59042	alpha-conotoxin Ep
8	22	22.9	16	2 G49039	T-cell receptor be
9	21	21.9	12	2 T46794	hypothetical prote
10	21	21.9	13	2 S08575	botulinum neurotox
11	21	21.9	16	2 I52266	aldehyde dehydroge
12	20	20.8	8	2 S71919	alcohol dehydrogen
13	20	20.8	9	2 A12872	transaldolase (EC
14	20	20.8	14	2 FT0077	proteochondroitin c
15	20	20.8	14	2 S29486	GTP-binding protei
16	20	20.8	15	2 S32677	nitrogenase cofact
17	20	20.8	15	2 PA0009	seed storage prote
18	20	20.8	17	2 D22595	sebolditin IV - Am
19	19	19.8	9	2 FT0272	Ig heavy chain CRD
20	19	19.8	9	2 A42266	peptidylglycine mo
21	19	19.8	10	2 PH0895	T-cell receptor be
22	19	19.8	11	4 PC2124	aminotransferase c
23	19	19.8	14	2 PH1627	Ig H chain V-D-J r
24	19	19.8	15	2 FT0095	H ₂ -transporting tw
25	19	19.8	15	2 S36889	ribosomal protein
26	19	19.8	17	2 S20490	photosystem II chl
27	18	18.8	7	2 S08606	hypothetical prote
28	18	18.8	10	2 FT0284	Ig heavy chain CRD
29	18	18.8	10	2 S27873	hypothetical prote

```

30 18 18.8 12 2 B61497 seed protein ws-17
31 18 18.8 13 2 G56046 urinary tract ston
32 18 18.8 14 2 I64815 carbonic anhydrase
33 18 18.8 14 2 PH1347 Ig heavy chain DJ
34 18 18.8 14 2 PH1625 Ig H chain V-D-J r
35 18 18.8 14 2 A41589 25K elastin-bindin
36 18 18.8 14 2 PA0007 lectin B1 - Psopho
37 18 18.8 15 2 I49407 placental calcium-
38 18 18.8 15 2 FT0222 Ig heavy chain CDR
39 18 18.8 15 2 PH1310 Ig heavy chain DJ
40 18 18.8 15 2 PA0005 lectin A1 - Psopho
41 18 18.8 15 2 PA0006 lectin A3 - Psopho
42 18 18.8 15 2 PA0008 lectin B2 - Psopho
43 18 18.8 16 2 A59046 alpha-conotoxin MI
44 18 18.8 16 2 PH1778 T cell receptor al
45 18 18.8 17 1 A61339 vesiculakinin 1 - e

```

ALIGNMENTS

RESULT 1

A61612
allatostatin - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A61612
R:Kramer, S.G.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A:Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.
A:Reference number: A61612; MUID:92052112; PMID:1946359
A:Accession: A61612
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <KRA>
A:Cross-references: UNIPROT:P42559
C:Keywords: neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

Qy 1 FEHCNFDVTV 10
Db 4 FRCQYFNPIS 13

```

RESULT 2

PC2215
fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment
N:Alternate names: alpha-fibrinogenase A2
C:Species: Crotalus atrox (western diamondback rattlesnake)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PC2215
R:Hung, C.C.; Chlou, S.H.
Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
A:Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamondback viper.
A:Reference number: PC2214; MUID:94296418; PMID:8024586
A:Accession: PC2215
A:Molecule type: protein
A:Residues: 1-15 <HUN>
A:Cross-references: UNIPROT:Q9PRW3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase

Query Match 26.0%; Score 25; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

Qy 2 EHCNFDND 8
Db 4 FRCQYFNPIS 13

```

Db 5 DECNINE 11

RESULT 3
H56046
urinary tract stone matrix protein 10, 42K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: H56046
R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A;Description: Isolation, characterization and sequence of stone proteins.
A;Reference number: A56046
A;Accession: H56046
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BIN>
A;Cross-references: UNIPROT:Q7M4P7

Query Match 25.0%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HCNFNDV 9
| | | |
| | | |

Db 2 HSYFNDL 8

RESULT 4
A11497
transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)
C;Species: Pichia jadinii, Candida utilis
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A11497
R;Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A;Title: Isolation of a peptide containing a histidinyl-cysteinyl sequence from the actin
A;Reference number: A11497; MUID:75145197; PMID:1092268
A;Accession: A11497
A;Molecule type: protein
A;Residues: 1-9 <TSO>
A;Cross-references: UNIPROT:PI7441
C;Keywords: transferase

Query Match 24.0%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCN 5
| | |
| | |

Db 4 HCN 6

RESULT 5
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C;Species: Synechococcus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: PS0371
R;Rhie, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A;Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning and
A;Reference number: JS0694; MUID:92201692; PMID:1551590
A;Accession: PS0371
A;Molecule type: DNA
A;Residues: 1-14 <RHI>
A;Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match 24.0%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DVTTTLR 14

Db 7 DVTGRLQ 13
| | | | |
| | | | |

RESULT 6
A61117
somatostatin precursor processing enzyme (EC 3.4.21.-) - American goosfish (fragment)
C;Species: Lophius americanus (American goosfish)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 13-Sep-1996
C;Accession: A61117
R;Mackin, R.B.; Noe, B.D.; Spiess, J.
Endocrinology 129, 2263-2265, 1991
A;Title: Identification of a somatostatin-14-generating propeptide converting enzyme as
A;Reference number: A61117; MUID:92007528; PMID:1680673
A;Accession: A61117
A;Molecule type: protein
A;Residues: 1-17 <MAC>
A;Experimental source: pancreatic islets
C;Superfamily: kexin; subtilisin homology
C;Keywords: hydrolase; serine proteinase

Query Match 24.0%; Score 23; DB 2; Length 17;
Best Local Similarity 27.3%; Pred. No. 2.1e+03;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTTLR 15
| | | | |
| | | | |

Db 4 NNDIEVNMKD 14

RESULT 7
A59042
alpha-conotoxin Epi - cone shell (Conus episcopatus)
C;Species: Conus episcopatus (bishop's cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: A59042
R;Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.C.
J. Biol. Chem. 273, 15667-15674, 1998
A;Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that selecti
A;Reference number: A59042; MUID:98288307; PMID:9624161
A;Accession: A59042
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <LOU>
A;Cross-references: UNIPROT:P56638
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot
F;1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
F;2-8,3-16/Disulfide bonds: #status experimental
F;15/Binding site: sulfate (Tyr) (covalent) #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.9%; Score 22; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFND 8
| | | |
| | | |

Db 8 CNMNN 12

RESULT 8
G49039
T-cell receptor beta chain V-D-J-C region (V beta 4, J beta 2.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: G49039
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: G49039
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Note: Sequence extracted from NCBI backbone (NCBIP:90719)
C;Keywords: T-cell receptor

Query Match 22.9%; Score 22; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRE 15
: : : : :
DB 1 CSVEDGTGRTGE 12

RESULT 9
T46794
hypothetical protein [imported] - Haloarcula marismortui (fragment)
C;Species: Haloarcula marismortui
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T46794

FEBS Lett. 267, 193-198, 1990
A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and
A;Reference number: S10731; MUID:90336772; PMID:2143141

A;Accession: T46794
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-12 <ARN>
A;Cross-references: UNIPROT:P10971; EMBL:X55311; NID:G43610; PID:G43611

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 LRENE 17
: : : : :
DB 8 LQENE 12

RESULT 10
S08575
botulinum neurotoxin type E - Clostridium botulinum (strain Alaska E-43) (fragment)
C;Species: Clostridium botulinum
A;Variety: strain Alaska E-43
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: S08575

R;Schmidt, J.J.; Sathyanarayanan, V.; DasGupta, B.R.
Arch. Biochem. Biophys. 238, 544-548, 1985
A;Title: Partial amino acid sequences of botulinum neurotoxins types B and E.
A;Reference number: S07128; MUID:85197963; PMID:3888113

A;Accession: S08575
A;Molecule type: protein
A;Residues: 1-13 <SCH>
A;Cross-references: UNIPROT:Q00496

A;Experimental source: strain Alaska E-43
F;1-13/Product: botulinum neurotoxin E light chain (fragment) #status predicted <LIG>

Query Match 21.9%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NFND 8
: : : : :
DB 7 NYND 10

RESULT 11
I52226
aldehyde dehydrogenase (EC 1.1.1.1) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I52226
R;Harper, K.; Jones, D.E.

Biochem. Biophys. Res. Commun. 152, 940-947, 1988
A;Title: Characterization of a functional recombinant rat liver aldehyde dehydrogenase: I
A;Reference number: I52226; MUID:88209084; PMID:3284529
A;Accession: I52226

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-16 <RES>
A;Cross-references: UNIPROT:Q63039; GB:M29320; NID:G202853; PIDN:AAA40722.1; PID:G202854
C;Keywords: oxidoreductase

Query Match 21.9%; Score 21; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTTLRE 15
: : : : :
DB 3 SISDTVKRARE 13

RESULT 12
S71919
alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71919
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim. Biophys. Acta 1296, 41-46, 1996
A;Title: Proteolytic activation of grass carp (Ctenopharyngodon idellus) liver alcohol de
A;Reference number: S71919; MUID:96350418; PMID:8765227

A;Accession: S71919
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <TSU>
A;Cross-references: UNIPROT:Q7LZ46
A;Note: the source is designated Ctenopharyngodon idellus
C;Keywords: NAD; oxidoreductase

Query Match 20.8%; Score 20; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDVTTR 12
: : : : :
DB 1 SDPTTR 6

RESULT 13
A12872
transaldolase (EC 2.2.1.2) I - yeast (Pichia jadinii) (fragment)
C;Species: Pichia jadinii, Candida utilis
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A12872
R;Sun, S.C.; Joris, L.; Tsolas, O.
Arch. Biochem. Biophys. 178, 69-78, 1977
A;Title: Purification and crystallization of transaldolase isozyme I and evidence for di
A;Reference number: A12872; MUID:77110646; PMID:556924

A;Accession: A12872
A;Molecule type: protein
A;Residues: 1-9 <SUN>
A;Cross-references: UNIPROT:P17440
C;Keywords: transferase

Query Match 20.8%; Score 20; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCN 5
: : : : :
DB 4 HCB 6

RESULT 14
PT0077

proteochondroitin core protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: PT0077
R;Marcum, J.A.; Thompson, M.A.
Biochem. Biophys. Res. Commun. 175, 706-712, 1991
A;Title: The amino-terminal region of a proteochondroitin core protein, secreted by aorta from human bone.

A;Reference number: PT0077; MUID:91207372; PMID:2018513
A;Accession: PT0077
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <MAR>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 20.8%; Score 20; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 FEHCNFDVT 10
|||
Db 3 FEQKGFDFT 12

RESULT 15

S29486
GTP-binding protein o-rab3 - electric ray (Discopyge ommata) (fragment)
C;Species: Discopyge ommata
C;Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S29486
R;Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicles
A;Reference number: S29485; MUID:93154521; PMID:8428634
A;Accession: S29486
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <VOL>

Query Match 20.8%; Score 20; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 NFNDV 9
|||
Db 8 NFNAV 12

Search completed: June 8, 2005, 11:08:54
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:46:13 ; Search time 166 Seconds

(without alignments)
52.442 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFNDVTTLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 8390

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	28	29.2	15	1 ALLS MANSE	P42559 manduca sex
2	28	29.2	16	2 Q7BW21	Q7BW21 incn plasm
3	27	28.1	13	2 Q8WMM1	Q8WMM1 sus scrofa
4	25	26.0	15	1 VSP3 AGKHP	P80899 agkistrodon
5	25	26.0	15	2 Q9PRW2	Q9PRW2 crotalus at
6	25	26.0	15	2 Q9PRW3	Q9PRW3 crotalus at
7	24	25.0	9	2 Q14715	Q14715 homo sapien
8	24	25.0	13	2 Q7M4P7	Q7M4P7 homo sapien
9	24	25.0	15	2 P78482	P78482 homo sapien
10	24	25.0	16	2 Q9AXV9	Q9AXV9 brassica ol
11	24	25.0	16	2 Q9AXW2	Q9AXW2 brassica na
12	24	25.0	16	2 Q6J071	Q6J071 hepatitis b
13	24	25.0	17	2 Q79DJ7	Q79DJ7 bacillus th
14	23.5	24.5	14	2 Q7IGT8	Q7IGT8 andrena bro
15	23	24.0	9	1 TAL3 PICUA	P17441 pichia jadi
16	23	24.0	12	2 Q7YNG4	Q7YNG4 bassia hyss
17	23	24.0	12	2 Q9FSA9	Q9FSA9 silene aega
18	23	24.0	13	2 P97622	P97622 rattus norv
19	23	24.0	14	2 Q55326	Q55326 synchococc
20	23	24.0	17	1 JHBP FLAVG	P56675 platyrepia
21	22.5	23.4	14	2 Q71GK0	Q71GK0 andrena ref
22	22	22.9	9	2 Q6LEH2	Q6LEH2 homo sapien
23	22	22.9	10	1 UPA9 HUMAN	P30095 homo sapien
24	22	22.9	12	2 Q81VF0	Q81VF0 homo sapien
25	22	22.9	16	1 CXAL CONEP	P56638 conus episc
26	22	22.9	16	2 Q77922	Q77922 oreochromis
27	22	22.9	17	2 Q7RDP8	Q7RDP8 plasmodium
28	22	22.9	17	2 Q6RSJ1	Q6RSJ1 coxiella bu
29	22	22.9	17	2 Q9QEX2	Q9QEX2 human immu
30	21.5	22.4	14	2 Q71G57	Q71G57 andrena aff
31	21.5	22.4	14	2 Q71GK2	Q71GK2 andrena wil

32	21.5	22.4	14	2 Q71GK4	Q71GK4 andrena nas
33	21.5	22.4	14	2 Q71GL4	Q71GL4 andrena n.
34	21.5	22.4	14	2 Q71GM4	Q71GM4 andrena 'vi
35	21.5	22.4	14	2 Q71GM6	Q71GM6 andrena eri
36	21.5	22.4	14	2 Q71GM8	Q71GM8 andrena mel
37	21.5	22.4	14	2 Q71GN2	Q71GN2 andrena are
38	21.5	22.4	14	2 Q71GN4	Q71GN4 andrena and
39	21.5	22.4	14	2 Q71GN6	Q71GN6 andrena lin
40	21.5	22.4	14	2 Q71GN8	Q71GN8 andrena ill
41	21.5	22.4	14	2 Q71GP0	Q71GP0 andrena vic
42	21.5	22.4	14	2 Q71GP2	Q71GP2 andrena niv
43	21.5	22.4	14	2 Q71GP6	Q71GP6 andrena car
44	21.5	22.4	14	2 Q71GQ0	Q71GQ0 andrena mis
45	21.5	22.4	14	2 Q71GQ2	Q71GQ2 andrena cre

ALIGNMENTS

RESULT 1

ALLS_MANSE STANDARD; PRT; 15 AA.
AC P42559;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Allatostatin (Mas-AS).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;

OC Sphingidae; Sphinginae; Manduca.

OX NCBI_TaxID=7130;

RN [1]

RP SEQUENCE.

RC TISSUE=Head;

RX MEDLINE=92052112; PubMed=1946359;

RA Kramer S.J., Toschi A., Miller C.A., Kataoka H., Quistad G.B.,

Li J.P., Carney R.L., Schooley D.A.;

RT "Identification of an allatostatin from the tobacco hornworm Manduca

sexta.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).

CC -I- FUNCTION: Strongly inhibits juvenile hormone biosynthesis in vitro

CC by the corpora allata from fifth-stadium larvae and adult females.

CC -I- SIMILARITY: Belongs to the allatostatin family.

DR PIR; A61612; A61612.

KW Direct protein sequencing; Neuropeptide; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.

SQ SEQUENCE 15 AA; 1908 MW; 1605B77CDEBC838E CRC64;

Query Match 29.2%; Score 28; DB 1; Length 15;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFNDVT 10

Db 4 FRQCYFNPS 13

RESULT 2

Q7BW21 PRELIMINARY; PRT; 16 AA.
ID Q7BW21

AC Q7BW21; 2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE TraIH (Fragment).

GN Name=traIH;

OS incn plasmid pKM101.

OC other sequences; broad host range plasmids.

OX NCBI_TaxID=192122;

RN [1]

RP SEQUENCE FROM N.A.

RA Woodgate R.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF000361; AAB5810.1; -;
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1791 MW; 49BCB8E5ECBD5CE7 CRC64;
 Query Match 29.2%; Score 28; DB 2; Length 16;
 Best Local Similarity 55.8%; Pred. No. 1.2e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 8 DVTITRLREN 16
 :||| :||
 Db 3 DITITRQN 11
 RESULT 3
 Q8WMM1 PRELIMINARY; PRT; 13 AA.
 ID Q8WMM1
 AC Q8WMM1
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Calpain-like protease (Fragment).
 GN Name=capn6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Capica S., Maspuet M., Rohrer G.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ429142; CAD22106.1; -;
 DR GO; GO:0008233; F:peptidase activity; IEA.
 KW Protease.
 FT NON_TER 1 1
 NON_TER 13 13
 FT SEQUENCE 13 AA; 1586 MW; 6C8D83C06AB72CB CRC64;
 QY 6 FNDVITRLRE 15
 :||| :|||
 Db 4 FSEVPVQLRE 13
 RESULT 4
 VSP3_AGKHP STANDARD; PRT; 15 AA.
 ID VSP3_AGKHP
 AC P80899;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ancrod (EC 3.4.21.74) (Venombin A) (Protein C activator) (ACC-C) (Fragment).
 OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC Tissue=Venom;
 RA Hong S.;
 RL Submitted (FEB-1997) to Swiss-Prot.
 CC -!- FUNCTION: Thrombin-like snake venom serine protease. Activates protein C [By similarity].
 CC -!- CATALYTIC ACTIVITY: Selective cleavage of Arg-|-Xaa bond in fibrinogen, to form fibrin, and release fibrinopeptide A. The specificity of further degradation of fibrinogen varies with species origin of the enzyme.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Snake venom subfamily.
 DR InterPro; IPR001254; Peptidase S1.
 DR PROSITE; PS0240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1642 MW; 03EFE10227CD8CDA CRC64;
 Query Match 26.0%; Score 25; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 3.4e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EHCNFD 8
 :||| :||
 Db 5 DECNIINE 11
 RESULT 5
 Q9PRW2 PRELIMINARY; PRT; 15 AA.
 ID Q9PRW2
 AC Q9PRW2
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE Alpha-FIBRINOGENASE isoform A3 (Fragment).
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94296418; PubMed=8024586;
 RA Hung C.C., Chiou S.H.;
 RT "Isolation of multiple isoforms of alpha-fibrinogenase from the Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence RT homology with ancrod, an antithrombotic agent from Malayan viper.";
 RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
 SQ SEQUENCE 15 AA; 1656 MW; 03EFE10227DS2FDA CRC64;
 Query Match 26.0%; Score 25; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 3.4e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EHCNFD 8
 :||| :||
 Db 5 DECNIINE 11
 RESULT 6
 Q9PRW3 PRELIMINARY; PRT; 15 AA.
 ID Q9PRW3
 AC Q9PRW3
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Alpha-FIBRINOGENASE isoform A3 (Fragment).
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94296418; PubMed=8024586;
 RA Hung C.C., Chiou S.H.;
 RT "Isolation of multiple isoforms of alpha-fibrinogenase from the Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence RT homology with ancrod, an antithrombotic agent from Malayan viper.";

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RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
DR PIR: PC2215; PC2215
SQ SEQUENCE 15 AA; 1640 MW; 03EFE10227CA12DA CRC64;

Query Match      26.0%; Score 25; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EHCNFND 8
Db : ||| :
5 DECINE 11

RESULT 7
Q14715 PRELIMINARY; PRT; 9 AA.
AC Q14715;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Keratin 14 (Fragment).
GN Name=KRT14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92005680; PubMed=1717157; DOI=10.1016/0092-8674(91)90051-Y;
RA Coulombe P., Hutton M., Letai A., Hebert A., Fuchs E.;
RT "Point mutations in human keratin 14 genes of epidermolysis bullosa simplex patients: genetic and functional analyses.";
RL Cell 66:1301-1311(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95072587; PubMed=7526926;
RA Yamanishi K., Matsuki M., Konishi K., Yasuno H.;
RT "A novel mutation of Leri22 to Phe at a highly conserved hydrophobic residue in the helix initiation motif of keratin 14 in epidermolysis bullosa simplex.";
RL Hum. Mol. Genet. 3:1171-1172(1994).
DR GO: GO:0005882; C:intermediate filament; NAS.
KW Keratin.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1138 MW; BE300AA449C456D6 CRC64;

Query Match      25.0%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NFND 8
Db : ||| :
4 NFND 7

RESULT 8
Q7M4P7 PRELIMINARY; PRT; 13 AA.
AC Q7M4P7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Urinary tract stone matrix protein 10, 42K (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Binette J.P., Binette M.B., Gawinowicz M.A., Kendrick N.;
RL Submitted (FEB-1995) to the PIR data bank.

DR PIR: H56046; H56046. 1
FT NON TER 1 13
SQ SEQUENCE 13 AA; 1483 MW; 0A219099F5D32AA4 CRC64;

Query Match      25.0%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HCNFNDV 9
Db : ||| :
2 HSYFNDL 8

RESULT 9
P78482 PRELIMINARY; PRT; 15 AA.
AC P78482;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE APOB protein (Fragment).
GN Name=APOB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88018019; PubMed=3659919;
RA Chen S.-H., Habib G., Yang C.-Y., Gu Z.-W., Lee B.R., Weng S.-A.,
RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
RA Gotto A.M.Jr., Li W.-H., Chan L.;
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in-frame stop codon.";
RL Science 238:363-366(1987).
DR EMBL: M18036; AAA51754.1; -.
DR PIR: A27850; LPHUB.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1842 MW; 9172790C16559AE8 CRC64;

Query Match      25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 NFNDVTRLR 14
Db : ||| :
2 NFNEKLSQLQ 11

RESULT 10
Q9AXV9 PRELIMINARY; PRT; 16 AA.
AC Q9AXV9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Phytochrome A (Fragment).
GN Name=PHYA-BO-1;
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12582899;
RA Fourmann M., Barret P., Froger N., Baron C., Charlot F., Delourme R.,
RA Brunel D.;
RT "From Arabidopsis thaliana to Brassica napus: development of amplified consensus genetic markers (ACGM) for construction of a gene map.";
RL Theor. Appl. Genet. 105:1196-1206(2002).
DR EMBL: AF229417; AAK00689.1; -.

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DR GO: GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
DR GO: GO:0009585; P:ired, far-red light phototransduction; IEA.
KW Phytochrome.
FT NON_TER 1 16
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1819 MW; 04C0F9AD5DDFBF0F CRC64;
Query Match 25.0%; Score 24; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 5.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 8 DVTRLREN 16
Db 5 DIVQRMLEN 13
RESULT 11
Q9AXW2 ID Q9AXW2 PRELIMINARY; PRT; 16 AA.
AC Q9AXW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Phytochrome A (Fragment).
GN Names=BN-PHYA-1;
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12582899;
RA Fournann M., Barret P., Froger N., Baron C., Charlot F., Delourme R.,
RA Brunel D.;
RT "From Arabidopsis thaliana to Brassica napus: development of amplified
RT consensus genetic markers (ACGM) for construction of a gene map.";
RL Theor. Appl. Genet. 105:1196-1206(2002).
DR EMBL; AF229413; AAK0685.1; -.
DR GO: GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
DR GO: GO:0009585; P:ired, far-red light phototransduction; IEA.
KW Phytochrome.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1791 MW; D390F9AD5DDFBF1D CRC64;
Query Match 25.0%; Score 24; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 5.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 8 DVTRLREN 16
Db 5 DIVQRMLEN 13
RESULT 12
Q6JQ71 ID Q6JQ71 PRELIMINARY; PRT; 16 AA.
AC Q6JQ71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15184419;
RA Sitnik R., Rebello Pinho J.R., Bertolini D.A., Bernardini A.P.,
RA Da Silva L.C., Carrilho F.J.;
RT "Hepatitis B virus genotypes and precore and core mutants in Brazilian
RT patients.";

RL J. Clin. Microbiol. 42:2455-2460(2004).
DR EMBL; AY29569; AAQ95940.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1896 MW; 6C1E698806A8E77B CRC64;
Query Match 25.0%; Score 24; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FEHCNFND 8
Db 9 FKDCLEFKD 16
RESULT 13
Q79DJ7 ID Q79DJ7 PRELIMINARY; PRT; 17 AA.
AC Q79DJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CytA (Fragment).
GN Name=cytA;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95247658; PubMed=7730255;
RA Dervyn E., Poncet S., Klier A., Rapoport G.;
RT "Transcriptional regulation of the cryIVD gene operon from Bacillus
RT thuringiensis subsp. israelensis.";
RL J. Bacteriol. 177:2283-2291(1995).
DR EMBL; S78174; AAB34195.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2052 MW; 085F1686F7987A08 CRC64;
Query Match 25.0%; Score 24; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 HCNFNDV 9
Db 6 HCPLEDI 12
RESULT 14
Q71GT8 ID Q71GT8 PRELIMINARY; PRT; 14 AA.
AC Q71GT8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena brooksi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205220;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504370; AAQ07711.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1754 MW; 7E93AE12A227BE5B CRC64;
Query Match 24.5%; Score 23.5; DB 2; Length 14;

Search completed: June 8, 2005, 11:08:11
Job time : 168 secs

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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:45:08 ; Search time 156 Seconds
(without alignments)
42.147 Million cell updates/sec

Title: US-09-020-393b-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFNDVTTLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	44.8	15	8	ADR38586 Human CD5
2	38	39.6	16	4	AAB67300 Cytokine
3	36	37.5	14	4	AB556683 Human SNP
4	33.5	34.9	15	8	ADM33098 Human imm
5	33	34.4	16	6	ABP82501 G protein
6	32.5	33.9	16	3	AAY58596 Toxoplasm
7	32	33.3	14	7	ADC17406 Type IV c
8	32	33.3	14	7	ADC17402 Type IV c
9	32	33.3	14	8	ADRI8924 Human typ
10	32	33.3	14	8	ADRI8928 Human typ
11	32	33.3	15	2	AAR83971 Virus inf
12	32	33.3	15	8	ADK70613 Human inf
13	32	33.3	15	8	ADK70612 Human ery
14	32	33.3	15	8	ADK70576 Human ery
15	32	33.3	15	8	ADK70658 Human ery
16	32	33.3	15	8	ADN65159 HLA bindi
17	32	33.3	16	2	AAR70779 EPO neuro
18	32	33.3	16	8	ADI38855 Human ery
19	32	33.3	17	2	AAR30024 Cytokine
20	32	33.3	17	2	AAW66142 Proseposi
21	32	33.3	17	8	ADQ94321 Human pre
22	31	32.3	10	7	ADE28574 Human CD1
23	31	32.3	14	4	AAM97385 Human pep
24	31	32.3	15	5	ABB83992 Human pho
25	31	32.3	15	5	ABJ04349 Human col

26	31	32.3	15	8	ADK70657 Human ery
27	31	32.3	15	8	ADK70611 Human ery
28	31	32.3	15	8	ADK70590 Human ery
29	31	32.3	15	8	ADK70575 Human ery
30	31	32.3	17	5	ADE03016 Hybrid po
31	30	31.2	8	3	AAY61736 Cadherin-
32	30	31.2	9	2	AAY43797 Specific
33	30	31.2	9	3	AAY61739 Cadherin-
34	30	31.2	10	7	ADC17691 Type IV c
35	30	31.2	10	8	ADRI9213 Type IV c
36	30	31.2	12	4	AAB97334 Collagen
37	30	31.2	15	2	AAW41168 Metal-reg
38	30	31.2	15	5	AAW47726 Peptide B
39	30	31.2	15	8	ADP26440 Plasmodiu
40	30	31.2	16	2	AAW41167 Metal-reg
41	30	31.2	16	6	ABP59517 Frd3 prot
42	29	30.2	9	2	AAW49475 Human leu
43	29	30.2	10	7	ADC17694 Type IV c
44	29	30.2	10	8	ADRI9216 Type IV c
45	29	30.2	12	7	ADF10462 Serum alb

ALIGNMENTS

RESULT 1
ADR38586
ID ADR38586 standard; peptide; 15 AA.
XX AC ADR38586;
DT 18-NOV-2004 (first entry)
XX DE Human CD59 amino acids 36-50.
XX KW Human; CD59; protein glycation; diabetes mellitus; urine; immunogen;
XX KM blood sugar; glycaemic control.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Modified-site 6 /note= "Optionally Glycated"
XX PN US2004166531-A1.
XX PD 26-AUG-2004.
XX PF 16-APR-2001; 2001US-00835752.
XX PR 08-MAY-2000; 2000US-0203254P.
XX PA (HALP/) HALPERIN J.
XX PI Halperin J;
XX DR WPI; 2004-634394/61.
XX DT
XX PT Determining impact of blood sugar level on glycation levels in diabetic patient involves measuring level of lysine residue at specific position in glycated membrane protein associated with regulation of complement system.
XX PS Example 5; SEQ ID NO 1; 18pp; English.
XX CC The invention relates to determining the impact of blood sugar level on protein glycation levels in a subject involves measuring a level of lysine residue at position 41 in a glycated membrane protein CD59 (K41-glycated CD59) from a sample (e.g. urine). Also included are evaluating/selecting a treatment for regulating blood sugar levels (e.g. in a patient suffering from diabetes mellitus), determining regression, progression or onset of a condition caused by abnormal levels of glycated protein, treating a subject to reduce the risk of or progression of a

CC disorder associated with abnormally high levels of K41-glycated CD59, a
CC composition comprising isolated, pure or fragment of isolated K41-
CC glycated CD59.; and an agent that binds to K41-glycated CD59 but not to
CC K41-nonglycated CD59. The method is used to monitor glycaemic control in
CC a diabetic patient, and to select subject for therapy, to monitor onset,
CC progression and/or regression of diabetes or other diseases by monitoring
CC levels of glycated CD59 in subject. The method provides direct indication
CC of the level of the subject's glycaemic control thus effectively
CC measuring impacts of blood sugar levels or glycation levels. The glycated
CC CD59 can be detected in urine, thus obviating the need for a blood
CC sample. The present sequence is a peptide used to raise anti-CD59
CC antibodies, comprising amino acids 36-50 of human CD59.
XX
SQ Sequence 15 AA;
Query Match 44.8%; Score 43; DB 8; Length 15;
Best Local Similarity 87.5%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FEHCNFND 8
Db ||| ||||
7 FEHANFND 14
RESULT 2
AAB67300
ID AAB67300 standard; peptide; 16 AA.
XX
AC AAB67300;
XX
DT 20-APR-2001 (first entry)
XX
DE Cytokine peptide #6.
XX
KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.
XX
OS Homo sapiens.
XX
PN EP1072609-A2.
XX
PD 31-JAN-2001.
XX
PF 30-JUN-2000; 2000EP-00305504.
XX
PR 30-JUN-1999; 99JP-00185155.
XX
PA (SAKA/) SAKANAKA M.
PA (TANA/) TANAKA J.
PA (SATO/) SATO K.
XX
PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;
XX WPI; 2001-204263/21.
XX
XX Use of prosaposin-related peptides or derivatives as cytoprotective
PT agents, for suppressing apoptosis or apoptosis-like cell death.
XX
PS Disclosure; Page 12; 41pp; English.
XX
CC The present invention relates to use of a prosaposin-related peptide or
CC derivative, in the production of a medicament for use in preventing or
CC delaying cell death, or in promoting the expression of cell death
CC supporting gene product Bcl-XL. The invention is useful for preventing
CC the death of cells e.g. brain cells, neurons and cardiac muscle cells, in
CC vitro or ex vivo
XX
SQ Sequence 16 AA;
Query Match 39.6%; Score 38; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 EHCNFNDVT 11

Db |||: |: ||
2 EHCSLNENTT 11
RESULT 3
AAB56683
ID AAB56683 standard; peptide; 14 AA.
XX
AC AAB56683;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP related amino acid sequence SEQ ID NO:1248.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX WPI; 2001-355949/37.
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
PS Claim 1; Page 620; 674pp; English.
XX
CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 14 AA;
Query Match 37.5%; Score 36; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFNDVT 13
Db |||: |: ||
3 QHCSRNNFTMRL 14
RESULT 4
ADM33098
ID ADM33098 standard; peptide; 15 AA.

```

XX AC ADM33098;
XX DT 17-JUN-2004 (first entry)
XX DE Human immunodeficiency virus 1 cell entry inhibitor peptide #126.
XX DE anti-HIV; gene therapy; HIV-1; TAT; gp120; HIV-1 cell entry inhibitor;
XX KW M-tropic HIV-1; L-tropic HIV-1.
XX OS Human immunodeficiency virus 1.
XX PN WO2004024173-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-EP010162.
XX PR 13-SEP-2002; 2002EP-00020649.
XX PR 19-DEC-2002; 2002EP-00028510.
XX PA (CREA-) CREABILIS THERAPEUTICS SRL.
XX PI Bussolino F, Marchio S;
XX DR WPI; 2004-269894/25.
XX DE Use of inhibitors of the interaction between HIV-1 TAT protein and HIV-1
XX PT gp120 for inhibiting the entry of HIV-1 into a host cell for treating
XX PT infections caused by M-tropic or L-tropic HIV-1 strains.
XX PS Claim 21; SEQ ID NO 127; 87pp; English.
XX CC The invention relates to novel inhibitors of the interaction between HIV-
XX CC 1 TAT protein and HIV-1 gp120 which are useful for inhibiting the entry
XX CC of HIV-1 into a host cell. The inhibitors of the interaction between HIV-
XX CC 1 TAT protein and HIV-1 gp120 are useful for inhibiting the entry of HIV-
XX CC 1 into a host cell for treating infections caused by M-tropic or L-tropic
XX CC HIV-1 strains. This sequence represents a peptide derived from the HIV-1
XX CC TAR86 protein which is used as an inhibitor of HIV-1 entry into cells.
XX SQ Sequence 15 AA;
Query Match 34.9%; Score 33.5; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;
QY 4 CNFNDVTTLRLE 15
DB 1 CSFN-ITTEIRD 11
: : : : :
: : : : :

RESULT 5
ABP82501
ID ABP82501 standard; peptide; 16 AA.
XX AC ABP82501;
XX DT 04-MAR-2003 (first entry)
XX DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1174.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX KW G protein-coupled receptor modulator; antibody; immune-related disease;
XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX KW immunological-related cell proliferative disease; autoimmune disease;
XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX KW ulcer.

XX OS Homo sapiens.
XX PN WO200261087-A2.
XX PD 08-AUG-2002.
XX PF 19-DEC-2001; 2001WO-US050107.
XX PR 19-DEC-2000; 2000US-0257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burmer GC, Roush CL, Brown JP;
XX DR WPI; 2003-046718/04.
XX DE New isolated antigenic peptides e.g., for G protein-coupled receptors
XX PT (GPCR), useful for diagnosing and designing drugs for treating conditions
XX PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX PT autoimmune diseases.
XX PS Claim 1; Fig 2; 523pp; English.
XX CC The present invention describes antigenic peptides (I) comprising: (a)
XX CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX CC acids. Also described: (1) an assay for the detection of a particular G
XX CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX CC and (2) an isolated antibody having high specificity and high affinity or
XX CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX CC antibody against a particular GPCR, and in the production of specific
XX CC antibodies. The peptides and antibodies are also useful for detecting the
XX CC presence or absence of corresponding GPCRs. The antigenic peptides for
XX CC GPCRs and antibodies are useful for diagnosing and designing drugs for
XX CC treating immune-related diseases, growth-related diseases, cell
XX CC regeneration-related disease, immunological-related cell proliferative
XX CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
XX CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX CC any other disorder in which GPCRs are involved. The antibodies may be
XX CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX CC exemplification of the present invention
XX SQ Sequence 16 AA;
Query Match 34.4%; Score 33; DB 6; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 4 CNFNDVTTLRLENE 17
DB 1 CGLSNKENRLEENE 14
: : : : :
: : : : :

RESULT 6
AAYS8596
ID AAYS8596 standard; peptide; 16 AA.
XX AC AAYS8596;
XX DT 10-APR-2000 (first entry)
XX DE Toxoplasma gondii antigen SAG1 epitope #8.
XX KW SAG1; antigen; toxoplasmosis; subunit vaccine; Pichia pastoris; epitope;
XX KW antibody.

```

XX	Toxoplasma gondii.
OS	
XX	WO9966043-A1.
PN	
XX	
PD	23-DEC-1999.
XX	
PF	08-JUN-1999; 99WO-EP003957.
XX	
PR	12-JUN-1998; 98GB-00012773.
PR	15-APR-1999; 99GB-00008564.
XX	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA	
XX	Biemans R, Bollien A, Haumont M;
PI	WPI; 2000-106101/09.
XX	
DR	Method for production of toxoplasma antigen SAG1 for use in vaccines.
PT	
XX	Example 1; Page 14; 47pp; English.
PS	
XX	The invention relates to the recombinant production of the toxoplasma
CC	antigen SAG1 or a fragment thereof in the yeast Pichia pastoris. SAG1 is
CC	the major surface antigen of Toxoplasma gondii, an obligate intracellular
CC	protozoan parasite responsible for toxoplasmosis in mammals, including
CC	humans. SAG1 is anchored to the plasma membrane of T. gondii via a GPI
CC	(glycosylphosphatidylinositol) anchor, which is attached to the C-
CC	terminal anchor region (residues 308-336). The invention provides a
CC	truncated SAG1 protein, which lacks the anchor region and comprises amino
CC	acids 48-307, and a SAG1 protein N-terminally fused to a yeast secretion
CC	signal peptide. The SAG1 protein and its fragments can be used in the
CC	manufacture of a subunit vaccine for the prevention or treatment of
CC	toxoplasmosis in mammals. A live attenuated Toxoplasma vaccine is
CC	available, but cannot be administered to humans due to the risk of
CC	reversion of the attenuated strain to a virulent form. Prior art
CC	recombinant expression of SAG1 has been attempted in Escherichia coli,
CC	mammalian cells or S. cerevisiae, but has been associated with problems
CC	such as misfolding and insolubility, low yields of correctly folded SAG1,
CC	or heterogeneous protein production. In addition, purification of the
CC	native protein from tachyzoites is difficult and time-consuming, due to
CC	the GPI anchor. Sequences AA58595-Y58596 represent peptide epitopes of
CC	T. gondii SAG1, which were used to raise polyclonal antibodies in an
CC	exemplification of the present invention
XX	
SQ	Sequence 16 AA;
	Query Match 33.9%; Score 32.5; DB 3; Length 16;
	Best Local Similarity 43.8%; Pred. No. 4.1e+02;
	Matches 7; Conservative 2; Mismatches 4; Indels 3; Gaps 1
QY	4 CN---FNDVTRLEN 16 : :
Dd	1 CNEKSFKDILPKLTEN 16 :
RESULT 7	
ADCL7406	
ID	ADCL7406 standard; peptide; 14 AA.
XX	
AC	ADCL7406;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Type IV collagen NC1 domain related peptide SEQ ID NO:7.
XX	
KW	crystallised NC1 domain hexamer of type IV collagen;
KW	angiogenesis inhibitor; angiogenesis-mediated disease;
KW	tumour metastasis inhibitor; tumour growth inhibitor;
KW	endothelial cell interaction inhibitor;
KW	basal lamina membrane formation inhibitor; cytostatic; antiproliferative;
KW	anti-neurotic; ophthalmological; antiarteriosclerotic; antiulcer;
KW	endothelial cell adhesion inhibitor;

KW	endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
KW	ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
KW	blood-borne tumour.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FN	WO2003012122-A2.
XX	
PD	13-FEB-2003.
XX	
PF	26-JUL-2002; 2002WO-US023763.
XX	
PR	27-JUL-2001; 2001US-0308523P.
PR	29-OCT-2001; 2001US-0351289P.
PR	22-MAR-2002; 2002US-0366854P.
PR	03-JUN-2002; 2002US-0385362P.
XX	
PA	(UNIV) UNIV KANSAS MEDICAL CENT.
PA	(SUND/) SUNDARAMOORTHY M.
PA	(HUDS/) HUDSON B.
XX	
PI	Sundaramoorthy M, Hudson B;
XX	
DR	WPI; 2003-332730/31.
XX	
PT	New polypeptide, useful for treating an angiogenesis-mediated disease or
PT	condition consisting of glaucoma or blood-borne tumors or for inhibiting
PT	basal lamina membrane formation in cell or tissue development.
XX	
XX	Claim 5; SEQ ID NO 7; 168pp; English.
XX	
CC	The present invention describes a crystallised NC1 domain hexamer of type
CC	IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
CC	pharmaceutical composition comprising the polypeptide and a carrier; (3)
CC	inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
CC	disease or condition in a mammal; (5) inhibiting tumour metastasis or
CC	growth; (5) inhibiting endothelial cell interaction with the
CC	extracellular matrix in an animal tissue; (6) inhibiting basal lamina
CC	membrane formation in cell or tissue development; (7) a crystal of an NC1
CC	domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
CC	collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
CC	crystallised NC1 domain hexamer of type IV collagen (I) has cytostatic,
CC	antiproliferative, antianaemic, ophthalmological, antiarteriosclerotic and
CC	anticancer activities, and can be used as an inhibitor of angiogenesis,
CC	tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
CC	cell proliferation, and basal lamina assembly. A (I) polypeptide can be
CC	used for treating an angiogenesis-mediated disease or condition
CC	consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
CC	psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
CC	or for inhibiting basal lamina membrane formation in cell or tissue
CC	development. The methods are useful for inhibiting angiogenesis in
CC	tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
CC	cell interaction with the extracellular matrix in an animal tissue, and
CC	identifying inhibitors of type IV collagen assembly. The present sequence
CC	represents a peptide which is used in the exemplification of the present
CC	invention.
XX	
SQ	Sequence 14 AA;
	Query Match 33.3%; Score 32; DB 7; Length 14;
	Best Local Similarity 55.6%; Pred. No. 4.3e+02;
	Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0
Qy	1 FEHCNFDNV 9
	: :
Dd	2 FYCYNINEV 10
RESULT 8	
ADC17402	
ID	ADC17402 standard; peptide; 14 AA.
XX	

AC ABC17402;
XX
DT 18-DEC-2003 (first entry)
XX
DE Type IV collagen NC1 domain related peptide SEQ ID NO:3.
XX
KW crystallised NC1 domain hexamer of type IV collagen;
XX angiogenesis inhibitor; angiogenesis-mediated disease;
KW tumour metastasis inhibitor; tumour growth inhibitor;
KW endothelial cell interaction inhibitor;
KW basal lamina membrane formation inhibitor; cytostatic; antiproliferative;
KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
KW endothelial cell proliferation inhibitor;
KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
KW blood-borne tumour.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W02003012122-A2.
XX
XX 13-FEB-2003.
XX
XX 26-JUL-2002; 2002WO-US023763.
XX
XX 27-JUL-2001; 2001US-0308523P.
XX 29-OCT-2001; 2001US-0351289P.
XX 22-MAR-2002; 2002US-0366854P.
XX 03-JUN-2002; 2002US-0385362P.
XX
XX (UNIV) UNIV KANSAS MEDICAL CENT.
PA (SUND//) SUNDARAMOORTHY M.
PA (HDS//) HUDSON B.
XX
XX Sundaramoorthy M, Hudson B;
XX WPI; 2003-332730/31.
XX
XX New polypeptide, useful for treating an angiogenesis-mediated disease or
PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
PT basal lamina membrane formation in cell or tissue development.
XX
XX Claim 5; SEQ ID NO 3; 168pp; English.
XX
XX The present invention describes a crystallised NC1 domain hexamer of type
CC IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
CC growth; (5) inhibiting endothelial cell interaction with the
CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
CC membrane formation in cell or tissue development; (7) a crystal of an NC1
CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
CC crystallised NC1 domain hexamer of type IV collagen (I) has cytostatic,
CC antiproliferative, antianaemic, ophthalmological, antiarteriosclerotic and
CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
CC cell proliferation, and basal lamina assembly. A (I) polypeptide can be
CC used for treating an angiogenesis-mediated disease or condition
CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
CC or for inhibiting basal lamina membrane formation in cell or tissue
CC development. The methods are useful for inhibiting angiogenesis in
CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
CC cell interaction with the extracellular matrix in an animal tissue, and
CC identifying inhibitors of type IV collagen assembly. The present sequence
CC represents a peptide which is used in the exemplification of the present
XX invention.
XX
XX Sequence 14 AA;
SQ

Query Match 33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 66.7%; Pred No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FEHCNFNDV 9
Db 2 FLFCNVNDV 10
| | | | |
| | | | |

RESULT 9
ADRI8924
ID ADRI8924 standard; peptide; 14 AA.
XX
AC ADRI8924;
XX
DT 04-NOV-2004 (first entry)
XX
XX Human type IV collagen NC1 inter-CDSR alpha3 chain peptide.
XX
XX DE
XX
XX angiogenesis; angiogenesis-mediated disease; tumour metastasis;
KW tumour growth; type IV collagen; NC1 domain hexamer; angiogenic;
KW cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
KW vulnerary; antiulcer; fungicide; virucide; protozoacide; anti-HIV;
KW antiinflammatory; antianaemic; antiscikling; osteopathic; vasotropic;
KW gastrointestinal; antipsoriatic; antiatherosclerotic.
XX
XX Homo sapiens.
OS
XX
XX W02004067762-A2.
XX
XX 12-AUG-2004.
XX
XX 27-JAN-2004; 2004WO-US002187.
XX
XX 27-JAN-2003; 2003US-0443133P.
XX
XX (UNIV) UNIV KANSAS MEDICAL CENT.
XX
XX Sundaramoorthy M, Hudson B;
XX WPI; 2004-594218/57.
XX
XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
PT tumor metastasis, and tumor growth, involves contacting subject with
PT crystallized type IV collagen NC1 domain hexamer polypeptide.
XX
XX Disclosure; SEQ ID NO 3; 178pp; English.
XX
XX The invention relates to a novel method for inhibiting angiogenesis,
CC angiogenesis-mediated diseases or conditions, tumour metastasis, and
CC tumour growth, involving contacting a subject with a crystallised type IV
CC collagen NC1 domain hexamer polypeptide. A polypeptide of the invention
CC has angiogenic, cytostatic, antidiabetic, ophthalmological,
CC antirheumatic, antiarthritic, immunosuppressive, antiseborrheic, virucide,
CC dermatological, antibacterial, vulnerary, antiulcer, fungicide, antiscikling,
CC protozoacide, anti-HIV, antiinflammatory, antianaemic, antiscikling,
CC osteopathic, vasotropic, gastrointestinal, antirheumatic, and
CC antiatherosclerotic activity. The polypeptide inhibits assembly of type
CC IV collagen heterotrimers and hexamers. The method of the invention is
CC useful for inhibiting angiogenesis, angiogenesis-mediated diseases or
CC conditions, tumour metastasis and tumour growth. The angiogenesis-
CC mediated disease or condition is solid and blood-borne tumours, diabetic
CC retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal
CC neovascularisation, macular degeneration, corneal neovascularisation,
CC retinopathy of prematurity, corneal graft rejection, neovascular
CC glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis,
CC periorbital keratitis sicca, Sjogren's, acne rosacea, phlyctenulosis,
CC syphilis, Mycobacteria infections, lipid degeneration, chemical burns,
CC bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster
CC infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,
CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
CC lupus, polyarteritis, Wegeners sarcoidosis, scleritis, Steven's Johnson

CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
 CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
 CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
 CC Eales disease, Bechet's disease, myopia, optic pits, Stargardt disease,
 CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NCI domain hexamer.
 XX
 SQ Sequence 14 AA;

Query Match 33.3%; Score 32; DB 8; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.3e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNFDV 9
 | | | | |
 Db 2 FLFCNNDV 10

RESULT 10
 ADR18928
 ID ADR18928 standard; peptide; 14 AA.
 AC ADR18928;
 XX
 XX
 DT 04-NOV-2004 (first entry)
 DE Human type IV collagen NCI inter-CDSR alpha6 chain peptide.
 XX
 XX
 KW angiogenesis; angiogenesis-mediated disease; tumour metastasis;
 KW tumour growth; type IV collagen; NCI domain hexamer; angiogenic;
 KW cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
 KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
 KW vulnary; antiulcer; fungicide; virucide; protozoacide; anti-HIV;
 KW antiinflammatory; antianaemic; antisickling; osteopathic; vasotropic;
 KW gastrointestinal; antipsoriatic; antiatherosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX WO2004067762-A2.
 XX
 PD 12-AUG-2004.
 XX
 XX 27-JAN-2004; 2004WO-US0002187.
 XX
 PR 27-JAN-2003; 2003US-0443133P.
 XX
 PA (UNIV) UNIV KANSAS MEDICAL CENT.
 XX
 PI Sundaramoorthy M, Hudson B;
 XX
 XX WPI; 2004-594218/57.
 XX
 XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
 PT tumor metastasis, and tumor growth, involves contacting subject with
 PT crystallized type IV collagen NCI domain hexamer polypeptide.
 XX
 XX Disclosure; SEQ ID NO 7; 178pp; English.
 PS
 PS The invention relates to a novel method for inhibiting angiogenesis,
 CC angiogenesis-mediated diseases or conditions, tumor metastasis, and
 CC tumor growth, involving contacting a subject with a crystallised type IV
 CC collagen NCI domain hexamer polypeptide. A polypeptide of the invention
 CC has angiogenic, cytostatic, antidiabetic, ophthalmological,
 CC antirheumatic, antiarthritic, immunosuppressive, antiseborrheic,
 CC dermatological, antibacterial, vulnary, antiulcer, fungicide, virucide,
 CC protozoacide, anti-HIV, antiinflammatory, antianaemic, antisickling,
 CC osteopathic, vasotropic, gastrointestinal, antipsoriatic, and
 CC antiatherosclerotic activity. The polypeptide inhibits assembly of type

CC IV collagen heterotrimers and hexamers. The method of the invention is
 CC useful for inhibiting angiogenesis, angiogenesis-mediated diseases or
 CC conditions, tumour metastasis and tumour growth. The angiogenesis-
 CC mediated disease or condition is solid and blood-borne tumours, diabetic
 CC retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal
 CC neovascularisation, macular degeneration, corneal neovascularisation,
 CC retinopathy of prematurity, corneal graft rejection, neovascular
 CC glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis,
 CC pterygium, keratitis sicca, sjogren's, acne rosacea, phlyctenulosis,
 CC syphilis, Mycobacteria infections, lipid degeneration, chemical burns,
 CC bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster
 CC infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,
 CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
 CC lupus, polyarteritis, Wegeners sarcoidosis, scleritis, Steven's Johnson
 CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
 CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
 CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
 CC Eales disease, Bechet's disease, myopia, optic pits, Stargardt disease,
 CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NCI domain hexamer.
 XX
 SQ Sequence 14 AA;

Query Match 33.3%; Score 32; DB 8; Length 14;
 Best Local Similarity 55.6%; Pred. No. 4.3e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFDV 9
 | | | | |
 Db 2 FYCYNFV 10

RESULT 11
 AAR83971
 ID AAR83971 standard; peptide; 15 AA.
 XX AAR83971;
 XX
 XX 16-OCT-2003 (revised)
 DT 21-MAY-1996 (first entry)
 XX
 XX Virus infection factor N-terminal peptide from silkworm body fluid.
 DE
 XX Amino terminal; silkworm; virus infection factor; promoter; recombinant;
 KW high yield; body fluid.
 KW
 XX Samia cynthia ricini.
 OS
 XX JP07252298-A.
 PN
 XX 03-OCT-1995.
 PD
 XX 18-NOV-1994; 94JP-00308468.
 PF
 XX 22-NOV-1993; 93JP-00314038.
 XX
 XX (KATA) KATAKURA IND CO LTD.
 PA
 XX WPI; 1995-371176/48.
 DR
 XX Virus infection factor from silkworm body fluid - used to promote
 PT infection of insect cells with protein-expressing recombinant virus in
 PT culture medium.
 PS
 PS Claim 6; Page 2; 11pp; Japanese.
 XX
 XX AAR83791 is an amino-terminal peptide of a virus infection factor derived
 CC from heat-treated silkworm body fluid. The new virus infection factor

CC (VIF) is useful for promoting the infection of insect cells with
CC recombinant nuclear polyhedrosis virus. The virus having been recombined
CC with a useful protein-expressing gene. The insect cell can then be
CC cultured and the useful protein expressed at high yields. The new VIF has
CC a mol. wt. of approx. 15.2 kDa and an isoelectric point of 9 or higher.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 15 AA;

Query Match 33.3%; Score 32; DB 2; Length 15;
Best Local Similarity 87.5%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FNDVTTREL 13
||| |||||
Db 2 FNVVTTREL 9

RESULT 12
ADK70613
ID ADK70613 standard; peptide; 15 AA.
XX
AC ADK70613;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human erythropoietin (EPO) protein-related epitope peptide #45.
XX
KW erythropoietin; EPO; non-immunogenic; immunogenic; EPO manufacture;
XX erythropoietin manufacture; anaemia; human.
XX
OS Homo sapiens.
XX
PN WO2004018515-A2.
XX
PD 04-MAR-2004.
XX
PF 07-AUG-2003; 2003WO-EP008725.
XX
PR 09-AUG-2002; 2002EP-00017914.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Baker M, Carr FJ;
XX
DR WPI; 2004-226801/21.
XX
PT New modified human erythropoietin molecules with reduced immunogenicity,
PT useful in various therapeutic applications such as in the treatment of
PT anemia.

XX
PS Example 1; Page 25; 38pp; English.
XX
DB This invention relates to a novel modified molecule comprising the
XX biological activity of human erythropoietin (EPO) and being substantially
XX non-immunogenic or less immunogenic than any non-modified molecule having
XX the same biological activity in an individual when used in vivo. The
XX invention is useful for manufacturing a modified human erythropoietin
XX molecule. The modified EPO may be used in various therapeutic
XX applications, such as in the treatment of anaemia. The present sequence
XX is that of a human EPO epitope peptide which is related to the invention.
XX
SQ Sequence 15 AA;

Query Match 33.3%; Score 32; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
||| |:
Db 1 EHCSLNENIT 10

RESULT 13

ADK70612
ID ADK70612 standard; peptide; 15 AA.

XX
AC ADK70612;

XX
DT 20-MAY-2004 (first entry)

XX
DE Human erythropoietin (EPO) protein-related epitope peptide #44.

XX
KW erythropoietin; EPO; non-immunogenic; immunogenic; EPO manufacture;
XX erythropoietin manufacture; anaemia; human.

XX
OS Homo sapiens.

XX
PN WO2004018515-A2.

XX
PD 04-MAR-2004.

XX
PF 07-AUG-2003; 2003WO-EP008725.

XX
PR 09-AUG-2002; 2002EP-00017914.

XX
PA (MERE) MERCK PATENT GMBH.

XX
PI Baker M, Carr FJ;

XX
DR WPI; 2004-226801/21.

XX
PT New modified human erythropoietin molecules with reduced immunogenicity,
PT useful in various therapeutic applications such as in the treatment of
PT anemia.

XX
PS Example 1; Page 25; 38pp; English.

XX
DB This invention relates to a novel modified molecule comprising the
XX biological activity of human erythropoietin (EPO) and being substantially
XX non-immunogenic or less immunogenic than any non-modified molecule having
XX the same biological activity in an individual when used in vivo. The
XX invention is useful for manufacturing a modified human erythropoietin
XX molecule. The modified EPO may be used in various therapeutic
XX applications, such as in the treatment of anaemia. The present sequence
XX is that of a human EPO epitope peptide which is related to the invention.
XX
SQ Sequence 15 AA;

Query Match 33.3%; Score 32; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
||| |:
Db 4 EHCSLNENIT 13

RESULT 14

ADK70576
ID ADK70576 standard; peptide; 15 AA.

XX
AC ADK70576;

XX
DT 20-MAY-2004 (first entry)

XX
DE Human erythropoietin (EPO) protein-related epitope peptide #10.

XX
KW erythropoietin; EPO; non-immunogenic; immunogenic; EPO manufacture;
XX erythropoietin manufacture; anaemia; human.

XX
OS Homo sapiens.

XX
PN WO2004018515-A2.

XX
PD 04-MAR-2004.

XX 07-AUG-2003; 2003WO-EP008725.
XX
XX 09-AUG-2002; 2002EP-00017914.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Baker M, Carr FJ;
XX
XX WPI; 2004-226801/21.
XX
XX New modified human erythropoietin molecules with reduced immunogenicity,
PT useful in various therapeutic applications such as in the treatment of
PT anemia.
XX
XX Disclosure; Page 15; 38pp; English.
XX
XX This invention relates to a novel modified molecule comprising the
CC biological activity of human erythropoietin (EPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity in an individual when used in vivo. The
CC invention is useful for manufacturing a modified human erythropoietin
CC molecule. The modified EPO may be used in various therapeutic
CC applications, such as in the treatment of anaemia. The present sequence
CC is that of a human EPO epitope peptide which is related to the invention.
XX
XX Sequence 15 AA;
SQ

Query Match 33.3%; Score 32; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFNDVTT 11
|||:|:|
DB 4 EHCSLNNIT 13

Search completed: June 8, 2005, 11:05:19
Job time : 158 secs

CC biological activity of human erythropoietin (EPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity in an individual when used in vivo. The
CC invention is useful for manufacturing a modified human erythropoietin
CC molecule. The modified EPO may be used in various therapeutic
CC applications, such as in the treatment of anaemia. The present sequence
CC is that of a human EPO epitope peptide which is related to the invention.
XX
XX Sequence 15 AA;
SQ

Query Match 33.3%; Score 32; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFNDVTT 11
|||:|:|
DB 4 EHCSLNNIT 13

RESULT 15
ADK70658
ID ADK70658 standard; peptide; 15 AA.
XX
XX AC ADK70658;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human erythropoietin (EPO) protein-related epitope peptide #90.
XX
XX KW erythropoietin; EPO; non-immunogenic; immunogenic; EPO manufacture;
XX erythropoietin manufacture; anaemia; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004018515-A2.
XX
XX PD 04-MAR-2004.
XX
XX PF 07-AUG-2003; 2003WO-EP008725.
XX
XX PR 09-AUG-2002; 2002EP-00017914.
XX
XX PA (MERE) MERCK PATENT GMBH.
XX
XX PI Baker M, Carr FJ;
XX
XX DR WPI; 2004-226801/21.
XX
XX PT New modified human erythropoietin molecules with reduced immunogenicity,
PT useful in various therapeutic applications such as in the treatment of
PT anemia.
XX
XX PS Example 1; Page 27; 38pp; English.
XX
XX CC This invention relates to a novel modified molecule comprising the

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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:08:19 ; Search time 150 Seconds
(without alignments)
43.445 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96

Sequence: 1 FEHCNFNDVTRLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 300379

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match: 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	54.2	13	17	US-10-870-342A-4
2	52	54.2	16	17	US-10-870-342A-16
3	48	50.0	14	17	US-10-870-342A-23
4	43	44.8	14	17	US-10-870-342A-3
5	43	44.8	14	17	US-10-870-342A-10
6	43	44.8	15	11	US-09-835-752-1
7	43	44.8	15	16	US-10-833-581-1
8	40	41.7	13	17	US-10-870-342A-21
9	40	41.7	17	17	US-10-870-342A-17
10	36	37.5	14	16	US-10-813-638-1248
11	33	34.4	16	14	US-10-225-567A-1174
					Sequence 4, Appli
					Sequence 16, Appl
					Sequence 23, Appl
					Sequence 3, Appli
					Sequence 10, Appl
					Sequence 1, Appli
					Sequence 21, Appl
					Sequence 17, Appl
					Sequence 1248, Ap

12	32	33.3	14	14	US-10-206-699-3	Sequence 3, Appli
13	32	33.3	14	14	US-10-206-699-7	Sequence 7, Appli
14	32	33.3	16	15	US-10-455-697-3	Sequence 3, Appli
15	32	33.3	17	16	US-10-746-442-16	Sequence 16, Appl
16	31	32.3	15	9	US-09-989-919-123	Sequence 13, Appl
17	30	31.2	8	14	US-10-006-869-1594	Sequence 1594, Ap
18	30	31.2	8	15	US-10-395-032-1594	Sequence 1594, Ap
19	30	31.2	9	8	US-08-821-739A-1	Sequence 1, Appli
20	30	31.2	9	14	US-10-006-869-1597	Sequence 1597, Ap
21	30	31.2	9	15	US-10-395-032-1597	Sequence 1597, Ap
22	30	31.2	10	14	US-10-206-699-298	Sequence 298, Appl
23	30	31.2	16	16	US-10-672-282-11	Sequence 11, Appl
24	29	30.2	10	14	US-10-206-699-301	Sequence 301, Appl
25	29	30.2	11	10	US-09-754-831A-22	Sequence 22, Appl
26	29	30.2	11	17	US-10-671-317-22	Sequence 22, Appl
27	29	30.2	12	14	US-10-094-401-234	Sequence 234, Appl
28	29	30.2	12	15	US-10-462-262-202	Sequence 202, Appl
29	29	30.2	13	14	US-10-174-613-28	Sequence 28, Appl
30	29	30.2	14	14	US-10-206-699-4	Sequence 4, Appli
31	29	30.2	16	16	US-10-425-115-260737	Sequence 260737,
32	29	30.2	16	17	US-10-870-342A-38	Sequence 38, Appl
33	28.5	29.7	15	14	US-10-147-910-35	Sequence 35, Appl
34	28.5	29.7	16	14	US-10-062-710-39	Sequence 39, Appl
35	28	29.2	7	17	US-10-821-240A-233	Sequence 233, Appl
36	28	29.2	9	17	US-10-870-342A-25	Sequence 25, Appl
37	28	29.2	10	10	US-09-573-822C-387	Sequence 387, Appl
38	28	29.2	13	16	US-10-363-204-5	Sequence 5, Appli
39	28	29.2	14	14	US-10-206-699-2	Sequence 2, Appli
40	28	29.2	14	15	US-10-169-103-11	Sequence 11, Appl
41	28	29.2	15	14	US-10-283-423-182	Sequence 182, Appl
42	28	29.2	15	14	US-10-213-821-184	Sequence 184, Appl
43	28	29.2	15	17	US-10-870-342A-37	Sequence 37, Appl
44	28	29.2	15	17	US-10-486-234-16	Sequence 16, Appl
45	27	28.1	11	15	US-10-468-543-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-870-342A-4
; Sequence 4, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-4

Query Match 54.2%; Score 52; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFND 8
Db 6 FEHCNFND 13

RESULT 2
US-10-870-342A-16
; Sequence 16, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF

; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-16

Query Match 54.2%; Score 52; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
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Db 9 FEHCNFND 16

RESULT 3
US-10-870-342A-23
; Sequence 23, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-23

Query Match 50.0%; Score 48; DB 17; Length 14;
Best Local Similarity 87.5%; Pred. No. 0.67;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
| | | | |
Db 7 FEHCNFNE 14

RESULT 4
US-10-870-342A-3
; Sequence 3, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Lys is glycosylated
US-10-870-342A-3

Query Match 44.8%; Score 43; DB 17; Length 14;
Best Local Similarity 87.5%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
| | | | |
Db 6 FEHANFND 13

RESULT 5
US-10-870-342A-10
; Sequence 10, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-10

Query Match 44.8%; Score 43; DB 17; Length 14;
Best Local Similarity 87.5%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
| | | | |
Db 6 FEHANFND 13

RESULT 6
US-09-835-752-1
; Sequence 1, Application US/09835752
; Publication No. US20040166531A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/09/835,752
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-752-1

Query Match 44.8%; Score 43; DB 11; Length 15;
Best Local Similarity 87.5%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
| | | | |
Db 7 FEHANFND 14

RESULT 7
US-10-833-581-1
; Sequence 1, Application US/10833581
; Publication No. US20040219606A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/10/833,581
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/835,752
; PRIOR FILING DATE: 2001-04-16

; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-833-581-1

Query Match 44.8%; Score 43; DB 16; Length 15;
Best Local Similarity 87.5%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFD 8
Db 7 FEHANFND 14

RESULT 8

US-10-870-342A-21
; Sequence 21, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-21

Query Match 41.7%; Score 40; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNF 6
Db 8 FEHCNF 13

RESULT 9

US-10-870-342A-17
; Sequence 17, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-17

Query Match 41.7%; Score 40; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNF 6
Db 12 FEHCNF 17

RESULT 10

US-10-813-638-1248
; Sequence 1248, Application US/10813638
; Publication No. US20040235026A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/10/813,638
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 1248
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(0)
; OTHER INFORMATION: cSNP translation
US-10-813-638-1248

Query Match 37.5%; Score 36; DB 16; Length 14;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNENDVTTRL 13
Db 3 QHCNRNFTWRL 14

RESULT 11

US-10-225-567A-1174
; Sequence 1174, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1174
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1174

Query Match 34.4%; Score 33; DB 14; Length 16;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 CNFNDVTTRLRENE 17
Db 1 CGLSNKENRLEENE 14

RESULT 12

US-10-206-699-3
; Sequence 3, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.

```
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MEHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-3

Query Match          33.3%; Score 32; DB 14; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FEHCNFNDV 9
Db      2 FLFCNVNDV 10

RESULT 13
US-10-206-699-7
; Sequence 7, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MEHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-7

Query Match          33.3%; Score 32; DB 14; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FEHCNFNDV 9
Db      2 FYICNINEV 10

RESULT 14
US-10-455-697-3
; Sequence 3, Application US/10455697
; Publication No. US20040018978A1
; GENERAL INFORMATION:
; APPLICANT: Campana, Wendy Marie
; APPLICANT: Myers, Robert R
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; TITLE OF INVENTION: Use of erythropoietin and erythropoietin mimetics for the
; FILE REFERENCE: 6627-PA1090
; CURRENT APPLICATION NUMBER: US/10/455,697
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,286
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modified human sequence
US-10-455-697-3

Query Match          33.3%; Score 32; DB 15; Length 16;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 EHCNENDVTT 11
Db      1 EHCSLNNIT 10

RESULT 15
US-10-746-442-16
; Sequence 16, Application US/10746442
; Publication No. US20040121958A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; FILE REFERENCE: 07256/024001
; CURRENT APPLICATION NUMBER: US/10/746,442
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074
; PRIOR FILING DATE: FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/611,307
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US97/04143
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide Sequence (hEPO)
US-10-746-442-16

Query Match          33.3%; Score 32; DB 16; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 EHCNENDVTT 11
Db      2 EHCSLNNIT 11

Search completed: June 8, 2005, 11:21:20
Job time : 152 secs
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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:59:08 ; Search time 42 Seconds
(without alignments)
30.215 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58
Perfect score: 96
Sequence: 1 FEHCNFNDVTRLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	44.8	15	4	US-09-835-752-1
2	32	33.3	17	1	US-08-232-513A-11
3	32	33.3	17	3	US-09-231-159-16
4	32	33.3	17	3	US-08-611-307-16
5	30	31.2	8	3	US-09-187-859-1594
6	30	31.2	8	4	US-09-839-542B-1594
7	30	31.2	9	3	US-09-187-859-1597
8	30	31.2	9	4	US-09-839-542B-1597
9	30	31.2	16	2	US-08-758-621-21
10	30	31.2	16	3	US-09-107-858-21
11	30	31.2	16	4	US-09-579-174-21
12	29	30.2	11	6	5496552-8
13	29	30.2	11	6	5496552-8
14	29	30.2	14	2	US-08-460-309-23
15	29	30.2	14	2	US-08-125-077-23
16	29	30.2	14	6	5444158-4
17	29	30.2	14	6	5444158-4
18	28	29.2	13	3	US-08-908-371B-4
19	28	29.2	13	1	US-08-522-326-6
20	27.5	28.6	10	2	US-08-556-597-133
21	27	28.1	12	2	US-08-685-357B-12
22	27	28.1	12	3	US-08-952-568-20
23	27	28.1	12	4	US-09-532-709G-1
24	27	28.1	13	4	US-10-158-847-129
25	27	28.1	16	4	US-10-038-612-16
26	27	28.1	16	6	5194585-1
27	27	28.1	16	6	5194585-3

28	27	28.1	16	6	5194585-1	Patent No. 5194585
29	27	28.1	16	6	5194585-3	Patent No. 5194585
30	27	28.1	17	4	US-10-038-612-114	Sequence 114, App
31	26.5	27.6	15	1	US-08-218-025A-105	Sequence 105, App
32	26	27.1	11	3	US-09-224-785-22	Sequence 22, Appl
33	26	27.1	11	3	US-09-224-785-25	Sequence 25, Appl
34	26	27.1	11	4	US-09-756-594-22	Sequence 22, Appl
35	26	27.1	11	4	US-09-756-594-25	Sequence 25, Appl
36	26	27.1	12	1	US-07-778-233B-33	Sequence 33, Appl
37	26	27.1	12	1	US-07-963-321-33	Sequence 33, Appl
38	26	27.1	12	1	US-08-290-641-33	Sequence 33, Appl
39	26	27.1	12	1	US-08-548-540-33	Sequence 33, Appl
40	26	27.1	12	5	PCT-US96-09809-33	Sequence 33, Appl
41	26	27.1	14	2	US-08-413-708B-5	Sequence 5, Appl
42	26	27.1	14	3	US-09-192-048-24	Sequence 24, Appl
43	26	27.1	16	3	US-09-164-186-5	Sequence 5, Appl
44	26	27.1	16	4	US-09-700-993-9	Sequence 9, Appl
45	26	27.1	17	3	US-08-706-344C-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-835-752-1
; Sequence 1, Application US/09835752
; Patent No. 6835545
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/09/835,752
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-752-1

Query Match 44.8%; Score 43; DB 4; Length 15;
Best Local Similarity 87.5%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	FEHCNFND 8
Db	7	FEHNFND 14

RESULT 2
US-08-232-513A-11
; Sequence 11, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Proasoposin and Cytokine-Derived Peptides
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25


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; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1594
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-187-859-1594

Query Match      31.2%; Score 30; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CNFNDVT 10
DB      1 CQINDVT 7

RESULT 6
US-09-839-542B-1594
; Sequence 1594, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1594
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-839-542B-1594

Query Match      31.2%; Score 30; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CNFNDVT 10
DB      1 CQINDVT 7

RESULT 7
US-09-187-859-1597
; Sequence 1597, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-020-393b-3_copy_42_58.closed.ra1

; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-187-859-1597

Query Match      31.2%; Score 30; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CNFNDVT 10
DB      1 CQINDVT 7

RESULT 8
US-09-839-542B-1597
; Sequence 1597, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-839-542B-1597

Query Match      31.2%; Score 30; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CNFNDVT 10
DB      1 CQINDVT 7

RESULT 9
US-08-758-621-21
; Sequence 21, Application US/08758621
; Patent No. 5846821
; GENERAL INFORMATION:
; APPLICANT: Gueriot, Mary Lou, and Eide, David J.
; TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,578
; FILING DATE: 29-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
```

; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: DCI-099CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-758-621-21

Query Match 31.2%; Score 30; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDVTTLRENE 17
Db 3 NDVTLPKEDD 13
||||| :|::

RESULT 10
US-09-107-858-21
; Sequence 21, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Gueriot, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; EARLIER FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-21

Query Match 31.2%; Score 30; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDVTTLRENE 17
Db 3 NDVTLPKEDD 13
||||| :|::

RESULT 11
US-09-579-174-21
; Sequence 21, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Gueriot, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-21

Query Match 31.2%; Score 30; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDVTTLRENE 17
Db 3 NDVTLPKEDD 13
||||| :|::

RESULT 12
5496552-8
; Patent No. 5496552
; APPLICANT: KUBERASAMPATH, THANGAVEL; RUEGER, DAVID C.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,252
; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO: 8;
; LENGTH: 11
5496552-8

Query Match 30.2%; Score 29; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFD 8
Db 1 FLHCQFSE 8
||||| :|::

RESULT 13
5496552-8
; Patent No. 5496552
; APPLICANT: KUBERASAMPATH, THANGAVEL; RUEGER, DAVID C.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,252
; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO: 8;
; LENGTH: 11
5496552-8

Query Match 30.2%; Score 29; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFD 8
Db 1 FLHCQFSE 8
||||| :|::

RESULT 14

US-08-460-309-23

US-08-480-3023
; Sequence 23, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460.309

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994

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/ RECORD DATE: 21 DEC 1991
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/472,319
/ FILING DATE: 30-JAN-1990
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/919,951
/

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FILING DATE: 27-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9721

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear

Query Match 30.2%; Score 29; DB 2; Length 14;
Best Local Similarity 38.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 6; Indels

Qy	4	CN	FNDV	TRL	REN	16
		:	:	:		
Db	1	CS	IVD	IDT	NQ	13
		EE				

RESULT 15

US-08-125-077-23
; Sequence 23, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700

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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:32:41 ; Search time 29.6279 Seconds
(without alignments)
84.435 Million cell updates/sec

Title: US-09-020-393b-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAPSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR79:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	559	1 C9HU	complement C9 prec
2	52	37.1	3227	2 T37964	probable ubiquitin
3	49	35.0	135	2 PNO494	NAD ADP-ribosyltra
4	48	35.0	524	2 A29677	complement C9 prec
5	48	34.3	665	2 AG1117	transketolase homo
6	48	34.3	665	2 A11477	transketolase homo
7	48	34.3	666	2 AF0815	transketolase (EC
8	46	32.9	203	2 T30493	hypothetical prote
9	46	32.9	254	2 E84826	hypothetical prote
10	46	32.9	292	2 C70421	conserved hypotet
11	46	32.9	930	2 JX0368	inter-alpha-trypsi
12	46	32.9	1372	2 T25933	hypothetical prote
13	46	32.9	2144	2 T21712	hypothetical prote
14	45.5	32.5	661	2 C81822	topoisomerase IV s
15	45.5	32.5	661	2 D81055	hypothetical 39.2K
16	45	32.1	357	2 JQ2174	hypothetical prote
17	45	32.1	357	2 S27909	hypothetical prote
18	45	32.1	440	2 C84265	adenylosuccinate s
19	45	32.1	732	2 T18567	hypothetical prote
20	45	32.1	895	2 T49010	hypothetical prote
21	45	32.1	1189	2 T30319	Lian-Aal retrotran
22	45	32.1	1235	2 AC1728	ATP-dependent deox
23	44.5	31.8	290	2 AB1176	fructokinases homo
24	44.5	31.8	290	2 A11533	fructokinases homo
25	44.5	31.8	884	2 T18649	hypothetical prote
26	44.5	31.8	1002	2 T19226	hypothetical prote
27	44.5	31.8	1028	2 C88364	protein C13B4.1 [i
28	44	31.4	358	2 T44333	hypothetical prote
29	44	31.4	535	2 F41034	pyruvate dehydroge

30	44	31.4	535	2 F81847	dihydrolipoamide S
31	44	31.4	560	2 S42158	KREI1 protein - ve
32	44	31.4	659	2 B81082	transketolase NMB1
33	44	31.4	659	2- B81862	transketolase (EC
34	44	31.4	662	2 G89909	transketolase (imp
35	44	31.4	668	2 A46013	coagulation factor
36	44	31.4	670	2 A12223	transketolase (imp
37	44	31.4	678	2 A71287	probable cytoplasm
38	44	31.4	679	2 S54299	transketolase (EC
39	44	31.4	944	1 S48821	probable membrane
40	44	31.4	971	2 E96794	hypothetical prote
41	44	31.4	1210	2 C59431	centaurin, delta 2
42	43.5	31.1	117	2 H75165	hypothetical prote
43	43.5	31.1	739	2 F86337	F14O10.2 protein -
44	43.5	31.1	2550	2 B53435	vesicular transpor
45	43	30.7	199	2 B97180	probable Zn-depend

ALIGNMENTS

RESULT 1

C9HU

complement C9 precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence revision 17-Nov-2000 #text change 09-Jul-2004

C;Accession: A59363; I52400; A91029; A94019; S8647; A59364; A03208

R;Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.

A;Description: unpublished results, 1988, cited by GenBank

A;Reference number: A59363

A;Accession: A59363

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-559 <MAR1>

A;Cross-references: UNIPROT:P02748; GB:X02176; NID:G29580; PIDN:CAA26117.1; PID:G29581

R;Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.

Biochemistry 27, 6529-6534, 1988

A;Title: Relationships between the gene and protein structure in human complement compon

A;Reference number: I52400; MUID:89118250; PMID:3219351

A;Accession: I52400

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 62-159 <MAR2>

A;Cross-references: GB:J02833; NID:G179727; PIDN:AAAS1890.1; PID:G179728

R;Stanley, K.K.; Koehler, H.P.; Luzio, J.P.; Jackson, P.; Tschopp, J.

EMBO J. 4, 375-382, 1985

A;Title: The sequence and topology of human complement component C9.

A;Reference number: A91029; MUID:85257464; PMID:4018030

A;Accession: A91029

A;Molecule type: mRNA

A;Residues: 'S', 1-313, 315-559 <STA>

A;Cross-references: GB:X02176; NID:G29580

R;Discipio, R.G.; Gehring, M.R.; Podack, E.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H.

Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984

A;Title: Nucleotide sequence of cDNA and derived amino acid sequence of human complement

A;Reference number: A94019; MUID:85063778; PMID:6095282

A;Accession: A94019

A;Molecule type: mRNA

A;Residues: 2-12, 'X', 14-16, 'X', 18-42, 'R', 44-313, 315-416, 'P', 418-559 <DIS>

A;Cross-references: GB:K02766; NID:G179725; PIDN:AAAS1889.1; PID:G179726

R;Lengweiler, S.; Schaller, J.; Rickli, E.E.

FEBS Lett. 380, 8-12, 1996

A;Title: Identification of disulfide bonds in the ninth component (C9) of human compleme.

A;Reference number: S68647; MUID:96181657; PMID:8603752

A;Accession: S68647

A;Molecule type: protein

A;Residues: 34-47;52-59;69-87, 'X', 89-93, 'T', 94-98;106-113;118-131;136-145;180-181, 'X', 18

R;Witze-Schlomp, K.; Hobart, M.J.; Fernie, B.A.; Orren, A.; Wurzner, R.; Rittner, C.; Ka

Immunogenetics 48, 144-147, 1998

A;Title: Heterogeneity in the genetic basis of human complement C9 deficiency.

A;Reference number: A59364; MUID:98298010; PMID:9634479

A;Note: submitted to GenBank, September 1996


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Query Match          34.3%; Score 48; DB 2; Length 666;
Best Local Similarity 50.0%; Pred. No. 22;
Matches          9; Conservative          5; Mismatches          4; Indels          0; Gaps          0;

Qy      8 VSLAFSEISVGAEFNKDD 25
      |||::|::|::|::|
Db      123 VGLAIAERTLGAQFNRPD 140

RESULT 8
T30493
hypothetical protein ORF143 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30493
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.
Virolgy 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30493
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-203 <KUZ>
A:Cross-references: UNIPROT:Q9YMI5; EMBL:AF081910; NID:g3822234; PIDN:AAF70329.1

Query Match          32.9%; Score 46; DB 2; Length 203;
Best Local Similarity 38.5%; Pred. No. 13;
Matches          10; Conservative          4; Mismatches          6; Indels          6; Gaps          1;

Qy      1 CLGVHLDVSLAFSEISVGAEFNKDDC 26
      |||::|::|::|::|
Db      143 CEGGELDIDL-----VGRQFSANDC 162

RESULT 9
E84826
hypothetical protein At2g40200 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84826
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujita, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; T.
nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84826
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <STO>
A:Cross-references: UNIPROT:Q9XKE0; GB:AE002093; NID:g6598939; PIDN:AAF18734.1;
C:Genetics:
A:Gene: At2g40200
A:Map position: 2

Query Match          32.9%; Score 46; DB 2; Length 254;
Best Local Similarity 50.0%; Pred. No. 16;
Matches          9; Conservative          1; Mismatches          8; Indels          0; Gaps          0;

Qy      9 SLAFSEISVGAEFNKDDC 26
      ::|||::|::|::|
Db      36 NLGFSSSSGGNFPADDC 53

RESULT 10
C70421
conserved hypothetical protein aq_1392 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: C70421
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, V.
Nature 392, 353-358, 1998

```

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:9819666; PMID:9537320
A;Accession: C70421
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-292 <QOF>
A;Cross-references: UNIPROT:O67397; GB:AEO00738; NID:g2983801; PIDN:AAC07368.1; PID:g298298
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq 1392
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH13

Query Match 32.9%; Score 46; DB 2; Length 292;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LGYHLDVSLAFSEISVG 18
| | | | | : :
Db 261 LKVELPRLAFSAITLG 277

RESULT 11

JX0368

N;Alternate names: IHRP; plasma glycoprotein
C;Species: Homo sapiens (man)
C;Date: 22-Apr-1995 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0368; PC2355; S68457; S78548
R;Seguchi, K.; Tobeta, T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; Tomita, M.
J. Biochem. 117, 14-18, 1995
A;Title: Cloning and characterization of cDNA for inter-alpha-trypsin inhibitor family H
A;Reference number: JX0368; MUID:95293915; PMID:7775381
A;Accession: JX0368
A;Molecule type: mRNA
A;Residues: 1-930 <SAG1>
A;Cross-references: UNIPROT:Q14624; DDBJ:D38595; NID:G64887; PIDN:BAA07602.1; PID:gl483
A;Accession: PC2355
A;Molecule type: protein
A;Residues: 29-44; 48-55; 61-75; 99-111; 140-151; 163-169; 211-224; 246-267; 274-281; 296-329; 392-399
A;Experimental source: liver
R;Nishimura, H.; Kakizaki, I.; Muta, T.; Sasaki, N.; Pu, P.X.; Yamashita, T.; Nagasawa, F.EBS Lett. 357, 207-211, 1995
A;Title: cDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A;Reference number: S68457; MUID:95104473; PMID:7805892
A;Accession: S68457
A;Molecule type: mRNA
A;Residues: 1-84, 1'-86-113, 'S', 115-930 <NIS>
A;Cross-references: EMBL:D38535; NID:g624879; PIDN:BAA07536.1; PID:gl402590
A;Accession: S78548
A;Molecule type: protein
A;Residues: 29-45; 171-184; 211-239; 274-281; 301-315; 429-443; 488-502; 690-695; 697-700; 703-727-729
A;Experimental source: liver
C;Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha t
C;Function:
C;Description: highly sensitive to plasma kallikrein
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <Sig>
F;29-687/Product: inter-alpha trypsin inhibitor heavy chain-related protein #status predi
F;688-930/Domain: carboxyl-terminal propetide #status predicted <CTP>
F;81, 207, 517/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;666/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;696,702/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;701/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 32.9%; Score 46; DB 2; Length 930;
Best Local Similarity 64.3%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CLGYHLDVSLAFSE 14
| | | | |
Db 414 CLGFDFDVSYAFLE 427

A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-661 <PAR>
A;Cross-references: UNIPROT:Q9UT79; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8516
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene.parE; NM1941
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
C;Keywords: isomerase

Query Match 32.5%; Score 45.5; DB 2; Length 661;
Best Local Similarity 34.5%; Pred. No. 54;
Matches 10; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

Qy 2 LGVHLD-----VSLAFSEISVGAEFNKDD 25
:|:|:|:|:|:|:|:|:|:|:|:|
Db 78 VGLHPPEGVPVVELVFTRLHAGGKFNKDD 106

RESULT 15

D81055
topoisomerase IV chain B NMBl682 [imported] - Neisseria meningitidis (strain MC58 serogroup C)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81055
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.P.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xie, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Veith, T.; et al.
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: AB1000; UID:20175755; PMID:10710307
A;Accession: D81055
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-661 <YET>
A;Cross-references: UNIPROT:Q9JY77; GB:AE002518; GB:AE002098; NID:g7226928; PIDN:AAF4203
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMBl682
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:24:21 ; Search time 136.651 Seconds

(without alignments)

97.431 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAPSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	559	1 CO9 HUMAN	P02748 homo sapien
2	59.5	42.5	547	1 CO9 HORSE	P48770 equus cabal
3	57	40.7	554	1 CO9 RAT	Q62930 rattus norv
4	54	38.6	1050	2 Q8D083	Q8D083 yersinia pe
5	54	38.6	1075	2 Q66C38	Q66C38 yersinia ps
6	53	37.9	546	2 Q6YZN1	Q6YZN1 oryza sativ
7	53	37.9	668	2 Q7UZP8	Q7UZP8 prochloroco
8	53	37.9	1392	2 Q69Z29	Q69Z29 mus musculus
9	52	37.1	297	2 Q7ZWY2	Q7ZWY2 xenopus lae
10	52	37.1	557	1 CO9 RABIT	P48747 oryctolagus
11	52	37.1	666	2 Q8EQM3	Q8EQM3 oceanobacil
12	52	37.1	3227	1 PTR1 SCHPO	Q13834 schizosacch
13	51	36.4	146	2 Q6S4H9	Q6S4H9 human papil
14	51	36.4	1491	2 Q8C115	Q8C115 m mus muscu
15	50.5	36.1	511	2 Q7VWQ3	Q7VWQ3 bordetella
16	50.5	36.1	512	2 Q7WNV3	Q7WNV3 bordetella
17	50	35.7	303	2 Q9E231	Q9E231 neisseria g
18	50	35.7	326	2 Q51944	Q51944 neisseria g
19	50	35.7	326	2 Q51948	Q51948 neisseria g
20	50	35.7	326	2 Q9Z4K1	Q9Z4K1 neisseria g
21	50	35.7	327	2 Q9Z4L5	Q9Z4L5 neisseria g
22	50	35.7	930	2 Q8N3Q3	Q8N3Q3 homo sapien
23	50	35.7	1449	2 Q81VE3	Q81VE3 homo sapien
24	49	35.0	135	1 PPOL ONCWA	Q08824 oncorhynch
25	49	35.0	548	1 CO9 MOUSE	P06683 mus musculu
26	49	35.0	573	2 Q7Q2F2	Q7Q2F2 anopheles g
27	49	35.0	893	2 Q8PTI0	Q8PTI0 methanosarc
28	48	34.3	665	2 Q8YA23	Q8YA23 listeria mo
29	48	34.3	665	2 Q92E08	Q92E08 listeria in
30	48	34.3	665	2 Q723W3	Q723W3 listeria mo
31	48	34.3	666	2 Q8Z4S9	Q8Z4S9 salmonella

32	48	34.3	666	2	Q8ZN82	Q8ZN82 salmonella
33	48	34.3	669	2	Q8D1X4	Q8D1X4 wiggleswort
34	48	34.3	675	2	Q7SD09	Q7SD09 neurospora
35	48	34.3	675	2	Q63Q51	Q63Q51 burkholderi
36	48	34.3	690	2	Q62H05	Q62H05 burkholderi
37	47.5	33.9	162	1	SE15 RAT	Q923V8 rattus norv
38	47.5	33.9	3108	2	Q6FWS9	Q6FWS9 candida gla
39	47	33.6	176	2	Q8MNV6	Q8MNV6 caenorhabdi
40	47	33.6	241	2	Q917L2	Q917L2 drosophila
41	47	33.6	324	2	Q6BD05	Q6BD05 drosophila
42	47	33.6	324	2	Q6BD06	Q6BD06 drosophila
43	47	33.6	324	2	Q6BD08	Q6BD08 drosophila
44	47	33.6	324	2	Q6BD09	Q6BD09 drosophila
45	47	33.6	324	2	Q6BD16	Q6BD16 drosophila

ALIGNMENTS

RESULT 1

CO9_HUMAN ID CO9_HUMAN STANDARD; PRT; 559 AA.

AC P02748;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Complement component C9 precursor.

GN Name=C9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85257464; PubMed=4018030;

RA Stanley K.K., Kocher H.-P., Luzio J.P., Jackson P., Tschoop J.;

RT "The sequence and topology of human complement component C9.";

RL EMBO J. 4:375-382 (1985).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=liver;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP SEQUENCE OF 2-559 FROM N.A.

RX MEDLINE=85063778; PubMed=6095282;

RA Discipio R.G., Gehring M.R., Podack E.R., Kan C.C., Hugli T.E.,

RA Fey G.H.;

RT "Nucleotide sequence of cDNA and derived amino acid sequence of human

complement component C9.";

Proc. Natl. Acad. Sci. U.S.A. 81:7298-7302 (1984).

RN [4]

RP SEQUENCE OF 62-159 FROM N.A.

RX MEDLINE=89118250; PubMed=3219351;

RA Maraziti D., Eggertsen G., Fey G.H., Stanley K.K.;
 RT "Relationships between the gene and protein structure in human
 RL complement component C9."; [PubMed:10050415](http://www.ncbi.nlm.nih.gov/pubmed/10050415);
 RN Biochemistry 27:6529-6534(1988).
 RP [5]
 RP SEQUENCE OF 27-559 FROM N.A., AND VARIANT C9D GLY-119.
 RX MEDLINE=98298010; PubMed=9634479; DOI=10.1007/s002510050415;
 RA Witzel-Schloemp K., Hobart M.J., Fernie B.A., Orren A., Wuerzner R.,
 RL Ritter C., Kaufmann T., Schneider P.M.;
 RN "Heterogeneity in the genetic basis of human complement C9
 RT deficiency";
 RL Immunogenetics 48:144-147(1998).
 RN [6]
 RN 3D-STRUCTURE MODELING OF MEMBRANE-SPANNING DOMAIN (MSB).
 RP MEDLINE=90370039; PubMed=2395434; DOI=10.1016/0161-5890(90)90001-G;
 RA Peitsch M.C., Amiguet P., Guy R., Brunner J., Maizel J.V. Jr.,
 RL Tschopp J.;
 RN "Localization and molecular modelling of the membrane-inserted domain
 RT of the ninth component of human complement and perforin.";
 RL Mol. Immunol. 27:589-602(1990).
 RN [7]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=20020247; PubMed=10551839; DOI=10.1074/jbc.274.46.32786;
 RA Hofsteenge J., Blommestein M., Hess D., Furmanek A., Miroshnichenko O.;
 RL "The four terminal components of the complement system are C-
 RT mannosylated on multiple tryptophan residues.";
 RN J. Biol. Chem. 274:32786-32794(1999).
 RN [8]
 RP DISULFIDE BONDS.
 RX PubMed=8603752; DOI=10.1016/0014-5793(95)01541-8;
 RA Lengweiler S., Schaller J., Rickli E.E.;
 RL "Identification of disulfide bonds in the ninth component (C9) of
 RT human complement.";
 RN FEBS Lett. 380:8-12(1996).
 CC -1- FUNCTION: C9 is the final component of the complement system to be
 CC added in the assembly of the membrane attack complex. It is able
 CC to enter lipid bilayers, forming transmembrane channels.
 CC -1- PTM: Thrombin cleaves factor C9 to produce C9a and C9b.
 CC -1- DISEASE: Defects in C9 are a cause of component C9 deficiency
 CC (C9D) [MIM:120940]. Patients with C9D suffer from recurrent
 CC bacterial infections, predominantly from *Neisseria meningitidis*.
 CC -1- SIMILARITY: Belongs to the complement C6/C7/C8/C9 family.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.
 CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -----
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 CC -----
 DR EMBL; X02176; CAA26117.1; -.
 DR EMBL; BC020721; AAH20721.1; -.
 DR EMBL; K02766; AAA51889.1; -.
 DR EMBL; J02833; AAA51890.1; -.
 DR EMBL; Y08545; CAA69848.1; -.
 DR EMBL; Y08546; CAA69849.1; JOINED.
 DR EMBL; Y08547; CAA69849.1; JOINED.
 DR EMBL; Y08548; CAA69849.1; JOINED.
 DR EMBL; Y08549; CAA69849.1; JOINED.
 DR EMBL; Y08550; CAA69849.1; JOINED.
 DR EMBL; Y08551; CAA69849.1; JOINED.
 DR EMBL; Y08552; CAA69849.1; JOINED.
 DR EMBL; Y08553; CAA69849.1; JOINED.
 DR EMBL; Y08554; CAA69849.1; JOINED.
 DR PIR; A59363; C9HU.
 DR HSSP; Q07954; 1CR8.
 DR Genew; HGNC:1358; C9.
 DR H-InvDB; HIX0004829; -.
 DR MIM; 120940; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0019836; P:hemolysis; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR001862; MAC_perforin.
 DR InterPro; IPR000884; TSPL.
 DR Pfam; PF00057; Ldl_recept_a; 1.
 DR Pfam; PF01823; MACPF; 1.
 DR Pfam; PF00090; TSP_1; 1.
 DR PRINTS; PR00764; COMPLEMENTC9.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01209; LDLRA_1; 1.
 DR PROSITE; PS0068; LDLRA_2; 1.
 DR PROSITE; PS00279; MAC_PERFORIN; 1.
 DR PROSITE; PS0092; TSP1; 1.
 KW Complement alternate pathway; Complement pathway; Cytolysis;
 KW Disease mutation; EGF-like domain; Glycoprotein;
 KW Membrane attack complex; Plasma; Signal; Transmembrane.
 FT SIGNAL 1 21 Complement component C9.
 FT CHAIN 22 559 Complement component C9a.
 FT CHAIN 22 285 Complement component C9b.
 FT CHAIN 266 559 TSP type-1.
 FT DOMAIN 42 95 LDL-receptor class A.
 FT DOMAIN 99 136 Potential.
 FT TRANSMEM 314 330 Potential.
 FT TRANSMEM 335 354 EGF-like.
 FT DOMAIN 506 540 Cleavage (by thrombin).
 FT SITE 265 286
 FT DISULFID 43 78
 FT DISULFID 54 57
 FT DISULFID 88 94
 FT DISULFID 101 112
 FT DISULFID 107 125
 FT DISULFID 119 134
 FT DISULFID 142 181
 FT DISULFID 254 255
 FT DISULFID 380 405
 FT DISULFID 510 526
 FT DISULFID 513 528
 FT DISULFID 530 539
 FT CARBOHYD 48 48 C-linked (Man).
 FT CARBOHYD 51 51 C-linked (Man); partial.
 FT CARBOHYD 277 277 N-linked (GlcNAc. .) (Probable).
 FT CARBOHYD 415 415 N-linked (GlcNAc. .) (Probable).
 FT VARIANT 119 119 C -> G (in C9D).
 FT CONFLICT 43 43 /FTID=VAR_012648.
 FT CONFLICT 314 314 C -> R (in Ref. 3).
 FT CONFLICT 417 417 Missing (in Ref. 3).
 FT CONFLICT 417 417 T -> P (in Ref. 3).
 SQ SEQUENCE 559 AA; 63173 MW; 7403F6AD7B3ECE1 CRC64;
 Query Match 100.0%; Score 140; DB 1; Length 559;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLGYHLDSVLSAFSEISVGAEFNKDDC 26
 DB 380 CLGYHLDSVLSAFSEISVGAEFNKDDC 405
 |||||
 RESULT 2
 CO9_HORSE
 ID CO9_HORSE STANDARD; PRT; 547 AA.
 AC P48770;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Complement component C9 precursor.
 GN Name=C9;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
[1]
NCBI_taxid=9796;
SEQUENCE FROM N.A.
MEDLINE=95325619; PubMed=7541424;
Tomlinson S., Wang Y., Ueda E., Esser A.F.;
"Chimeric horse/human recombinant C9 proteins identify the amino acid
sequence in horse C9 responsible for restriction of hemolysis.";
J. Immunol. 155:436-444(1995).
CC CC -!- FUNCTION: C9 is the final component of the complement system to be
added in the assembly of the membrane attack complex. It is able
to enter lipid bilayers, forming transmembrane channels.
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- PM: Thrombin cleaves factor C9 to produce C9a and C9b.
CC CC -!- SIMILARITY: Belongs to the complement C6/C7/C8/C9 family.
CC CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC CC -!- SIMILARITY: Contains 1 TSP type-1 domain.

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CC EMBL: U19381; AAB16820.1; -.
DR HSPG; Q07954; LJ8E.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001862; MAC_perforin.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF01823; MACPF; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR00764; COMPLEMENTC9.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PSS0068; LDLRA_2; 1.
DR PROSITE; PS00279; MAC_PERFORIN; 1.
DR PROSITE; PS50092; TSPI; 1.
KW Complement alternate pathway; Complement pathway; Cytolysis;
KW EGF-like domain; Glycoprotein; Membrane attack complex; Plasma;
Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 547 Complement component C9.
FT DOMAIN 42 95 TSP type-1.
FT FT DOMAIN 99 136 LDL-receptor class A.
FT FT TRANSMEM 314 330 Potential.
FT FT TRANSMEM 335 354 Potential.
FT DOMAIN 506 540 EGF-like.
FT DISULFID 43 78 By similarity.
FT DISULFID 54 57 By similarity.
FT FT DISULFID 88 94 By similarity.
FT FT DISULFID 101 112 By similarity.
FT FT DISULFID 107 125 By similarity.
FT FT DISULFID 119 134 By similarity.
FT FT DISULFID 142 181 By similarity.
FT FT DISULFID 380 404 By similarity.
FT FT DISULFID 510 526 By similarity.
FT FT DISULFID 513 528 By similarity.
FT FT CARBOHYD 260 260 By similarity.
FT FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 451 451 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 547 AA; 62014 MW; 75E5PE961DE873B6 CRC64;

Query Match 42.5%; Score 59.5; DB 1; Length 547;
Best Local Similarity 46.2%; Pred. No. 1.6; Indels 1; Gaps 1;
Matches 12; Conservative 7; Mismatches 6;

```

Qy 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
Db 380 CLGFNLDSLK-DKYEVTAIKDKDC 404
||||:||||:||||:||||:
||||:||||:||||:||||:
||||:||||:||||:||||:
||||:||||:||||:||||:

RESULT 3
CO9_RAT STANDARD; PRT; 554 AA.
AC Q62930; Q62957;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Complement component C9 precursor.
GN Name=C9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RC MEDLINE=97355567; PubMed=9212048;
RA Lassiter H.A., Walz B.M., Wilson J.L., Jung E., Calisi C.R.,
RA Goldsmith L.J., Wilson R.A., Morgan B.P., Feldhoff R.C.;
RT "The administration of complement component C9 enhances the survival
RT of neonatal rats with Escherichia coli sepsis.";
RN Pediatr. Res. 42:128-136(1997).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Hinchliffe S.J., Van den Berg C.W., Rushmere N.K., Morgan B.P.;
RT "Cloning of rat C9: consequences for homologous restriction of
RT complement";
RN Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: C9 is the final component of the complement system to be
CC added in the assembly of the membrane attack complex. It is able
CC to enter lipid bilayers, forming transmembrane channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the complement C6/C7/C8/C9 family.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC -----
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CC -----
DR EMBL; U49071; AAB38023.1; -
DR EMBL; U52948; AAA96528.1; ALT_INIT.
DR HSSP; Q07954; IJ8E.
DR RGD; 620319; C9.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001862; MAC_perforin.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF000057; Ldl_recept_a; 1.
DR Pfam; PF01823; MACPF; 1.
DR Pfam; PF000090; TSP 1; 1.
DR PRINTS; PR00764; COMPLEMENTC9.
DR PROSITE; PS00022; EGF 1; 1
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PSS0068; LDLRA_2; 1.
DR PROSITE; PS00279; MAC_PERFORIN; 1.
DR PROSITE; PSS0092; TSP1; 1.
KW Complement alternate pathway; Complement pathway; Cytolysis;
KW EGF-like domain; Glycoprotein; Membrane attack complex; Plasma;
KW Signal; Transmembrane.
FT SIGNAL 1 20 Potential.

```

Query Match 42.5%; Score 59.5; DB 1; Length 547;
Best Local Similarity 46.2%; Pred. No. 1.6;
Matches 12; Conservative 7; Mismatches 6; Indels

```
FT CHAIN 21 554 Complement component C9.
FT DOMAIN 40 93 TSP type-1.
FT DOMAIN 97 134 LDL-receptor class A.
FT TRANSMEM 316 332 Potential.
FT TRANSMEM 337 356 Potential.
FT DOMAIN 515 549 EGF-like.
FT SITE 267 268 Cleavage (by thrombin).
FT DISULFID 41 76 By similarity.
FT DISULFID 52 55 By similarity.
FT DISULFID 86 92 By similarity.
FT DISULFID 99 110 By similarity.
FT DISULFID 105 123 By similarity.
FT DISULFID 117 132 By similarity.
FT DISULFID 140 179 By similarity.
FT DISULFID 382 413 By similarity.
FT DISULFID 519 535 By similarity.
FT DISULFID 522 537 By similarity.
FT DISULFID 539 548 By similarity.
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 409 409 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
FT CONFLICT 65 65 I -> M (in Ref. 2).
FT CONFLICT 300 300 K -> R (in Ref. 2).
SQ SEQUENCE 554 AA; 62280 MW; 9C885F76A1275649 CRC64;

Query Match 40.7%; Score 57; DB 1; Length 554;
Best Local Similarity 43.8%; Pred. No. 4;
Matches 14; Conservative 3; Mismatches 9; Indels 6; Gaps 1;

QY 1 CLGYHLDVSL-----AFSEISVGAEFNKDDC 26
Db 382 CLGFLNLDVSLYPLQTALEGPSTANVNHSDC 413

RESULT 4
Q8D083 PRELIMINARY; PRT; 1050 AA.
AC Q8D083;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative adhesin.
GN OrderedLocusNames=y2605;
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Staley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AB013862; AAM86159.1; -.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR003344; Big 1.
DR InterPro; IPR003535; Intimin.
DR InterPro; IPR008964; Invasin_intimin.
DR Pfam; PF02369; Big_1; 3.
DR PRINTS; PR01369; INTIMIN.
DR SMART; SM00634; BID_1; 3.
SQ SEQUENCE 1050 AA; 111967 MW; 7C215A33E9B013B5 CRC64;

Query Match 38.6%; Score 54; DB 2; Length 1050;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 2 LGYHL-----DVSLAFSEISVGAEFNKD 24
Db 181 LGYNLFVDHDASYSHTRIGVGAEGRD 207

RESULT 6
Q6YZN1 PRELIMINARY; PRT; 546 AA.
AC Q6YZN1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0426E02.8 (Hypothetical protein
DE B104G07.30).
GN Names=P0426E02.8; Synonyms=B104G07.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SASAKI T., Matsumoto T., Katayose Y.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA SASAKI T., Matsumoto T., Katayose Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
```

```
QY 2 LGYHL-----DVSLAFSEISVGAEFNKD 24
Db 181 LGYNLFVDHDASYSHTRIGVGAEGRD 207

RESULT 5
Q66C38 PRELIMINARY; PRT; 1075 AA.
AC Q66C38;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative invasin precursor.
GN ORFNames=YPTB1572;
OS Versinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnbusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20811.1; -.
DR InterPro; IPR003344; Big 1.
DR InterPro; IPR003535; Intimin.
DR InterPro; IPR008964; Invasin_intimin.
DR Pfam; PF02369; Big_1; 3.
DR PRINTS; PR01369; INTIMIN.
DR SMART; SM00634; BID_1; 3.
KW Signal.
FT SIGNAL 1 54 Potential.
SQ SEQUENCE 1075 AA; 114564 MW; AF94B11B71D4AB38 CRC64;

Query Match 38.6%; Score 54; DB 2; Length 1075;
Best Local Similarity 44.4%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 2 LGYHL-----DVSLAFSEISVGAEFNKD 24
Db 181 LGYNLFVDHDASYSHTRIGVGAEGRD 207

RESULT 6
Q6YZN1 PRELIMINARY; PRT; 546 AA.
AC Q6YZN1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0426E02.8 (Hypothetical protein
DE B104G07.30).
GN Names=P0426E02.8; Synonyms=B104G07.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SASAKI T., Matsumoto T., Katayose Y.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA SASAKI T., Matsumoto T., Katayose Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AP005520; BAD03752.1; -.
DR EMBL; AP005096; BAD03478.1; -.
DR InterPro; IPR004158; DUF247.
DR Pfam; PF03140; DUF247; 1.
KW Hypothetical protein.
SQ SEQUENCE 546 AA; 61147 MW; 9688ED4409BB7A4E CRC64;

Query Match 37.9%; Score 53; DB 2; Length 546;
Best Local Similarity 41.7%; Pred. No. 17;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGYHLDVSLAFSEISVGAEFNKDDC 25
Db 455 LGHGEVAKHFADLCKGAVFDADD 478

RESULT 7
Q7UZP8 PRELIMINARY; PRT; 668 AA.
AC Q7UZP8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transketolase [EC 2.2.1.1].
GN Name=tktA; Synonyms=cbt; OrderedLocusNames=PMW1610;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825699; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lameran J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572094; CAE20069.1; -.
DR HSSP; P23254; 1AYO.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004802; F:transketolase activity; IEA.
DR InterPro; IPR005478; Bactransketolase.
DR InterPro; IPR005476; Transketolase C.
DR InterPro; IPR005475; Transketolase CR.
DR InterPro; IPR005474; Transketolase N.
DR InterPro; IPR009014; Transketo_C_Like.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF00456; Transketolase_N; 1.
DR Pfam; PF02779; Transket_pyr; 1.
DR TIGRFAMs; TIGR00232; tkt_lase_bact; 1.
DR PROSITE; PS00801; TRANSKETOLASE_1; 1.
DR PROSITE; PS00802; TRANSKETOLASE_2; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 668 AA; 72987 MW; 70C7177DDF431FFB CRC64;

Query Match 37.9%; Score 53; DB 2; Length 668;
Best Local Similarity 52.6%; Pred. No. 20;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 8 VSLAFSEISVGAEFNKDDC 26
Db 130 VGLAIEAHLAAKFNKDDC 148

RESULT 8
Q69Z29 PRELIMINARY; PRT; 1392 AA.
AC Q69Z29;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE KIAA2028 protein (Fragment).
GN Name=KIAA2028;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R.P., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
CC 1- SIMILARITY: Contains 2 PH domains.
DR EMBL; AK173337; BAD32615.1; -.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM_
DR InterPro; IPR00857; MYTH4.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH-related.
DR Pfam; PF00784; MYTH4; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00139; MYTH4; 1.
DR SMART; SM00233; PH; 2.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS50003; PH DOMAIN; 2.
FT NON_TER 1
SQ SEQUENCE 1392 AA; 156192 MW; B7CC2971EEED711E CRC64;

Query Match 37.9%; Score 53; DB 2; Length 1392;
Best Local Similarity 43.5%; Pred. No. 42;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 YHLDVSLAFSEISVGAEFNKDDC 26
Db 812 YHLTAVAGSNINVGSEFQVLC 834

RESULT 9
Q7ZWY2 PRELIMINARY; PRT; 297 AA.
AC Q7ZWY2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MGS2879 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046655; AAH46655.1; -;
DR InterPro; IPR008978; HSP20 chap.
SQ SEQUENCE 297 AA; 33656 MW; FDI7E16D9BFC7C28 CRC64;

Query Match 37.1%; Score 52; DB 2; Length 297;
Best Local Similarity 43.5%; Pred. No. 13;
Matches 10; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 4 YHLDVSLAFSEI--SVGAENKDC 24
||||| : : : : :
DB 262 YHLDIFLPNIQVESGAENRDC 284

RESULT 10
ID CO9 RABIT STANDARD; PRT; 557 AA.
AC P48747;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Complement component C9 precursor.
GN Name=C9;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_TaxID=9986;
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-34.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=95181293; PubMed=7533152; DOI=10.1074/jbc.270.8.3483;
RA Huesler T., Lockert D.H., Kaufman K.M., Soderz J.M., Sims P.J.;
RT "Chimeras of human complement C9 reveal the site recognized by
RT complement regulatory protein CD59";
RL J. Biol. Chem. 270:3483-3486(1995).
CC -!- FUNCTION: C9 is the final component of the complement system to be
CC added in the assembly of the membrane attack complex. It is able
CC to enter lipid bilayers, forming transmembrane channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Thrombin cleaves factor C9 to produce C9a and C9b.
CC -!- SIMILARITY: Belongs to the complement C6/C7/C8/C9 family.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC [1]
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20055; AAC48459.1; -;
DR HSSP; Q07954; 1CR8.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001862; MAC_perforin.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF000057; Ldl_recept_a; 1.
DR Pfam; PF01823; MACPF; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PRO0764; COMPLEMENTC9.
DR PRINTS; PRO0261; LDLRECEPTOR.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00668; LDLRA_2; 1.
DR PROSITE; PS00279; MAC_PERFORIN; 1.
DR PROSITE; PS0092; TSPI; 1.
KW Complement alternate pathway; Complement pathway; Cytolysis;
KW Direct protein sequencing; EGF-like domain; Glycoprotein;
KW Membrane attack complex; Plasma; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 557 Complement component C9.
FT DOMAIN 42 95 TSP type-1.
FT DOMAIN 99 137 LDL-receptor class A.
FT TRANSMEM 319 335 Potential.
FT TRANSMEM 340 359 Potential.
FT DOMAIN 516 550 EGF-like.
FT DISULFID 43 78 By similarity.
FT DISULFID 54 57 By similarity.
FT DISULFID 88 94 By similarity.
FT DISULFID 101 113 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 120 135 By similarity.
FT DISULFID 143 182 By similarity.
FT DISULFID 385 414 By similarity.
FT DISULFID 520 536 By similarity.
FT DISULFID 538 549 By similarity.
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 282 282 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 424 424 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 557 AA; 62662 MW; FF4565FF8D1AB417 CRC64;

Query Match 37.1%; Score 52; DB 1; Length 557;
Best Local Similarity 36.7%; Pred. No. 25;
Matches 11; Conservative 8; Mismatches 7; Indels 4; Gaps 1;

QY 1 CLGYHLDVSLAF----SEISVGAENKDC 26
||||| : : : : :
DB 385 CLGFDLDSLNTPGKSLGSLTGQANKNC 414

RESULT 11
ID Q8EQM3 PRELIMINARY; PRT; 666 AA.
AC Q8EQM3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transketolase (EC 2.2.1.1).
GN Name=ktk; OrderedLocustNames=OB1672;
OS Oceanobacillus ihayensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;


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RP SEQUENCE FROM N.A.
RA Forslund O., Hradil B., Nordin P., Stenquist B., Kirnbauer R.,
RA Slupetsky K., Lindelof B., Dillner J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY468416; AAR30925.1; -.
DR GO: GO:0019028; C-viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; Late_protein_L1; 1.
DR PRINTS: PR00865; HPV_CAPSID_L1.
DR ProDom: PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16331 MW; 32190C2E457541EA CRC64;

Query Match 36.4%; Score 51; DB 2; Length 146;
Best Local Similarity 44.0%; Pred. No. 9.4;
Matches 11; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

OY 2 LGVHLDVSLAFSEISVGAEFNKDDC 26
Db 115 IGEHWDV----AKPCAGAQFNKGDC 135

RESULT 14
ID Q8C115 PRELIMINARY; PRT; 1491 AA.
AC DT 01-MAR-2003 (TrEMBLrel. 23, Created)
AC DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:483144IH15 product:hypothetical Serine-rich region/Band
DE 4.1 family/PH domain profile/Core domain in kinesin and myosin
DE motors/Pleckstrin homology (PH) domain containing protein, full insert
DE sequence.
GN Names=Plekhh2; Synonyms=A1256725;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 PH domains.
DR EMBL: AK029252; BAC26356.1; -.
DR HSSP: O08967; IFHX.
DR MGD; MGI:2146813; Plekh2.
DR GO: GO:0005856; C:cytoskeleton; IEA.
DR GO: GO:0003779; F:actin binding; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003774; F:motor activity; IEA.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR009065; FERM.
DR InterPro: IPR000857; MYTH4.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011036; PH-related.
DR Pfam: PF00784; MYTH4; 1.
DR Pfam: PF00169; PH; 1.
DR SMART: SM00295; B41; 1.
DR SMART: SM00139; MYTH4; 1.
DR SMART: SM00233; PH; 2.
DR PROSITE: PS50057; FERM 3; 1.
DR PROSITE: PS50003; PH_DOMAIN; 2.
DR Hypothetical protein.
KW SEQUENCE 1491 AA; 167749 MW; 1326DCD4F5E33018 CRC64;

Query Match 36.4%; Score 51; DB 2; Length 1491;
Best Local Similarity 43.5%; Pred. No. 94;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 4 YHLDVSLAFSEISVGAEFNKDDC 26
Db 911 YHLTVAAGSNINVGEFQLVC 933

RESULT 15
OYVTQ3
ID Q7VTQ3 PRELIMINARY; PRT; 511 AA.
AC DT 01-OCT-2003 (TrEMBLrel. 25, Created)
AC DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Bp3462;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-599 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cordero-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Gobie A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640421; CAB43725.1; -.
DR InterPro; IPR010799; Mlrc C.
DR InterPro; IPR009197; UCP0I2702.
DR Pfam; PF07364; DUF1485; 1.
DR Pfam; PF07171; Mlrc C; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 511 AA; 54878 MW; FF15CA71D998C599 CRC64;

Query Match 36.1%; Score 50.5; DB 2; Length 511;
Best Local Similarity 60.0%; Pred. No. 39;
Matches 12; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 2 LGYHLDVSLAFSEISVGAEF 21
DB 11 LGFHLE-SNAFSLSEADP 29

```

Search completed: June 8, 2005, 10:44:06
 Job time : 138.651 secs

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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:24:06 ; Search time 143.302 Seconds
(without alignments)
70.172 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp1980s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	27	2	AAU27328 Human C9
2	140	100.0	82	2	AAU27324 Human C9
3	140	100.0	474	8	ADR20062 Human imm
4	140	100.0	522	8	ABM83944 Human dia
5	140	100.0	522	8	ABM83943 Human dia
6	140	100.0	560	2	AAU18310 Human com
7	52	37.1	86	2	AAU27325 Rabbit C9
8	52	37.1	278	6	ABU43379 Protein e
9	52	37.1	561	2	AAU18311 Rabbit co
10	51	36.4	405	6	ABU21387 Protein e
11	50	35.7	1449	7	ADF55468 Human nov
12	49	35.0	276	6	ABU25340 Protein e
13	48.5	34.6	417	7	ABO71707 Pseudomon
14	48	34.3	63	8	ABO55228 Human gen
15	48	34.3	304	5	ABP39673 Staphyloc
16	48	34.3	304	8	ADSO5775 Staphyloc
17	48	34.3	363	8	ADN19420 Bacterial
18	48	34.3	662	6	ABU16669 Protein e
19	48	34.3	663	6	ADA35154 Acinetoba
20	48	34.3	665	5	ABB48204 Listeria
21	48	34.3	666	6	ABU47082 Protein e
22	48	34.3	690	6	ABU22543 Protein e
23	48	34.3	1263	4	AAU72637 Exophiala
24	48	34.3	1263	5	AAE26387 Exophiala
25	48	34.3	1263	6	ABG75930 Fumonisin

ALIGNMENTS

RESULT 1

AAU27328
ID AAU27328 standard; peptide; 27 AA.

XX AAU27328;
AC AC
DT 05-NOV-1999 (first entry)
XX
DE Human C9 protein fragment (residues 359-384).

XX CD59 mediated complement; human; CD59 protein; C9 protein; mimetic;
XX tumour therapy; complement-mediated inflammation; immune disorder;
XX immunovascularitis; rheumatoid arthritis; scleroderma; C5b-9 complex.

OS Homo sapiens.

XX WO9940115-A2.

XX 12-AUG-1999.

XX 09-FEB-1999; 99WO-US002802.

XX 09-FEB-1998; 98US-00020393.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX (BLOO-) BLOOD CENT RES FOUND INC.

PI Sims PJ;

XX WPI; 1999-527301/44.

XX Compounds modulating CD59 mediated complement activity, for treatment of,
XX e.g. immunovascularitis.

XX Example 2; Page 36; 75pp; English.

XX The invention relates to compounds modulating CD59 mediated complement
XX activity. It provides (i) molecules structurally mimicking human CD59
XX amino acid residues 42-58 (region which serves as binding site for CD59 -
XX C9 interactions) when they are in a spatial orientation which can inhibit
XX the formation of the human C5b-9 complex. These mimetics specifically
XX bind to amino acid residues 359-384 of human C9. (ii) molecules
XX structurally mimicking C9 amino acids 359-384 when they are in a spatial
XX orientation which can promote the formation of the C5b-9 complex.
XX Compounds that mimic CD59 can be used to increase CD59 inhibition of C5b-
XX 9 complex assembly. This is especially useful in patients in need of
XX suppression of complement-mediated inflammation, e.g. immune disorders
XX and diseases such as immunovascularitis, rheumatoid arthritis, scleroderma.

Abu07914 Exophiala
Abu62941 E. spinif
Abb67215 Drosophil
Abb67214 Drosophil
Abb59606 Drosophil
Abu43213 Protein e
Aau44799 Propionib
Abm41318 Propionib
Aau32845 Novel hum
Ads23643 Bacterial
Adp29306 Human sec
Adp29311 Human sec
Adg75681 Human pro
Adp40374 Staphyloc
Adso5003 Staphyloc
Adj71943 Human PMW
Add49035 Human NOV
Abm83742 Human dia
Abm83741 Human dia
Add49037 Human NOV

26 48 34.3 1263 6 ABU07914
27 48 34.3 1263 6 ABU62941
28 47 33.6 241 4 ABB67215
29 47 33.6 391 4 ABB67214
30 47 33.6 391 4 ABB59606
31 47 33.6 662 6 ABU43213
32 46 32.9 214 4 AAU44799
33 46 32.9 214 6 ABM41318
34 46 32.9 339 4 AAU32845
35 46 32.9 344 8 ADS23643
36 46 32.9 502 8 ADP29306
37 46 32.9 502 8 ADP29311
38 46 32.9 648 7 ADG75681
39 46 32.9 675 5 ABP40374
40 46 32.9 675 8 ADS05003
41 46 32.9 748 8 ADJ71943
42 46 32.9 843 7 ADD49035
43 46 32.9 845 8 ABM83742
44 46 32.9 873 8 ABM83741
45 46 32.9 882 7 ADD49037

<hr/>					
ABM83943	ID	ABM83943 standard; protein; 522 AA.			
XX	AC	ABM83943;			
XX	DT	18-NOV-2004 (first entry)			
XX	DE	Human diagnostic and therapeutic pprotein SEQ ID NO:4192.			
XX	KW	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.			
XX	OS	Homo sapiens.			
XX	PN	WO2004023973-A2.			
XX	PD	25-MAR-2004.			
XX	PP	12-SEP-2003; 2003WO-US028227.			
XX	PR	12-SEP-2002; 2002US-0410259P.			
XX	PR	12-SEP-2002; 2002US-0410260P.			
XX	PA	(INCY-) INCYTE CORP.			
XX	PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;			
XX	PI	Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;			
XX	PI	Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;			
XX	PI	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;			
XX	PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;			
XX	PI	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;			
XX	PI	Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;			
XX	PI	Patury S, Shi X, Suarez CJ;			
XX	DR	WPI: 2004-329368/30.			
XX	DR	N-PSDB; ACN42595.			
XX	PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful			
XX	PT	in diagnosing a condition, disease or disorder associated with human			
XX	PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or			
XX	PT	in gene mapping.			
XX	PS	Claim 27; Page; 190pp; English.			
XX	CC	The invention relates to novel diagnostic and therapeutic polynucleotides			
XX	CC	selected from one of the 2722 sequences defined in the specification. A			
XX	CC	polynucleotide of the invention may have a use in gene therapy. The human			
XX	CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be			
XX	CC	used to diagnose a particular condition, disease or disorder associated			
XX	CC	with human molecules, e.g. cell proliferative disorders,			
XX	CC	autoimmune/inflammatory disorder, developmental disorder, endocrine			
XX	CC	disorder, neurological disorders, gastrointestinal disorders, or			
XX	CC	infections caused by virus, bacteria, fungi or parasite. The dithp			
XX	CC	molecules may also be used in genetic mapping, in identifying individuals			
XX	CC	from minute biological samples, in detecting single nucleotide			
XX	CC	polymorphisms, as molecular weight markers, and for somatic or germline			
XX	CC	gene therapy. The present sequence represents a dithp protein of the			
XX	CC	invention. Note: The sequence data for this patent is not represented in			
XX	CC	the printed specification, but was obtained in electronic format directly			
XX	CC	from WIPO at www.wipo.int/pct/en/sequences/listing.htm			
XX	SQ	Sequence 522 AA;			
XX	Query Match	100.0%; Score 140; DB 8; Length 522;			
XX	Best Local Similarity	100.0%; Pred. No. 4.7e-14;			
XX	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CLGYHLDVSLAFSEISVGAEFNKDDC 26			
DB	343	CLGYHLDVSLAFSEISVGAEFNKDDC 368			
RESULT 6					
AAM18310					

gene #28906.

11 proliferation: drug design.

PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA25257.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 49311; 1766pp; English.
 PS
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 405 AA;

 Query Match 36.4%; Score 51; DB 6; Length 405;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

 QY 3 GYHLDVSLAFSEISVGAEFNKD 24
 Db 210 GVSLEVQLATGNKKTGAEPND 231

 RESULT 11
 ADF55468
 ID ADF55468 standard; protein; 1449 AA.
 XX
 AC ADF55468;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 XX Human novel polypeptide #32.
 DE
 XX

KW human; brain disease; mental disorder.
 XX
 OS Homo sapiens.
 XX
 PN JP2003245081-A.
 XX
 PD 02-SEP-2003.
 XX
 PF 25-FEB-2002; 2002JP-00047501.
 XX
 PR 25-FEB-2002; 2002JP-00047501.
 XX
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
 XX
 XX WPI; 2003-857164/80.
 DR N-PSDB; ADF55419.
 DR
 XX New DNA derived from KG-1 cDNA library and encoded polypeptide, useful
 PT for treating mental disorders.
 PT
 XX Claim 4; SEQ ID NO 32; 401pp; Japanese.
 PS
 XX The invention relates to a DNA which encodes a novel polypeptide. A
 CC vector containing the DNA is useful as a reagent in estimation of
 CC standard substance. The antibody is useful for detecting the vector
 CC containing the DNA and for screening substances and compounds that
 CC interact specifically with the vector containing the DNA. The vector
 CC containing the DNA is used as a pharmaceutical, in treatment or as
 CC preventive agent with respect to disease e.g., brain diseases preferably
 CC mental disorders. The present sequence represents the amino acid sequence
 CC of a novel human polypeptide.
 XX
 SQ Sequence 1449 AA;

 Query Match 35.7%; Score 50; DB 7; Length 1449;
 Best Local Similarity 39.1%; Pred. No. 1.2e+02;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

 QY 4 YHLDVSLAFSEISVGAEFNKDDC 26
 Db 868 YHLTVAAGSNVNVGSEFEQLVC 890

 RESULT 12
 ABU25340
 ID ABU25340 standard; protein; 276 AA.
 XX
 AC ABU25340;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #10867.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Clostridium difficile.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 23-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 10:44:17 ; Search time 125.767 Seconds
(without alignments)
79.247 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	27	14	US-10-403-340-18
2	140	100.0	82	14	US-10-403-340-14
3	53	37.9	536	16	US-10-437-963-123986
4	52	37.1	86	15	US-10-403-340-15
5	52	37.1	278	15	US-10-282-122A-71303
6	51	36.4	405	15	US-10-282-122A-49311
7	49	35.0	276	15	US-10-282-122A-53264
8	48	34.3	63	14	US-10-029-386-28862
9	48	34.3	363	15	US-10-369-493-2073
10	48	34.3	662	15	US-10-282-122A-44593
11	48	34.3	666	15	US-10-282-122A-75006

12	48	34.3	690	15	US-10-282-122A-50467
13	48	34.3	1263	10	US-09-882-694-11
14	47	33.6	443	17	US-10-732-923-2707
15	47	33.6	662	15	US-10-282-122A-71137
16	46.5	33.2	1377	16	US-10-425-115-301836
17	46	32.9	46	16	US-10-425-115-317512
18	46	32.9	66	15	US-10-424-599-165510
19	46	32.9	124	16	US-10-767-701-58365
20	46	32.9	344	15	US-10-369-493-12876
21	46	32.9	843	15	US-10-336-603A-8
22	46	32.9	882	15	US-10-336-603A-10
23	46	32.9	900	15	US-10-336-603A-12
24	46	32.9	900	17	US-10-489-695-2
25	46	32.9	930	15	US-10-444-575-6
26	46	32.9	930	15	US-10-440-464-126
27	46	32.9	930	15	US-10-336-603A-6
28	46	32.9	930	17	US-10-344-307A-10
29	46	32.9	930	17	US-10-344-307A-12
30	46	32.9	1372	15	US-10-369-493-5971
31	45.5	32.5	623	15	US-10-389-566-1528
32	45.5	32.5	623	17	US-10-732-923-9786
33	45.5	32.5	661	15	US-10-282-122A-66034
34	45.5	32.5	848	16	US-10-437-963-114617
35	45.5	32.5	943	17	US-10-741-849-7309
36	45	32.1	50	16	US-10-425-115-288410
37	45	32.1	65	16	US-10-437-963-149891
38	45	32.1	366	16	US-10-437-963-164486
39	45	32.1	440	15	US-10-369-493-18601
40	45	32.1	542	15	US-10-377-079-78
41	44.5	31.8	86	16	US-10-767-701-57038
42	44.5	31.8	162	17	US-10-919-554-9
43	44.5	31.8	277	15	US-10-424-599-218729
44	44.5	31.8	434	15	US-10-369-493-14100
45	44.5	31.8	505	16	US-10-425-115-334893

ALIGNMENTS

RESULT 1

US-10-403-340-18
; Sequence 18, Application US/10403340
; Publication No. US20030166565A1
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: Compositions and Methods to Inhibit the
; CSb-9 Complex of Complement
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10403.340
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/020.393B
; FILING DATE: 03-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 170
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-403-340-18

Query Match 100.0%; Score 140; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.1e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
Db 2 CLGYHLDVSLAFSEISVGAEFNKDDC 27

RESULT 2

US-10-403-340-14
; Sequence 14, Application US/10403340
; Publication No. US20030166565A1
; GENERAL INFORMATION:

; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: Compositions and Methods to Inhibit the
; C5b-9 Complex of Complement

; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; St.

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/403,340

; FILING DATE: 27-Mar-2003

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/020,393B

; FILING DATE: 03-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMR# 170

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-873-8794

; TELEFAX: 404-873-8795

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 82 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-403-340-14

Query Match 100.0%; Score 140; DB 14; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
Db 26 CLGYHLDVSLAFSEISVGAEFNKDDC 51

RESULT 3

US-10-437-963-123986

; Sequence 123986, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 123986

; LENGTH: 536

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_26769C.1.pap

US-10-437-963-123986

Query Match 37.9%; Score 53; DB 16; Length 536;

Best Local Similarity 41.7%; Pred. No. 17;

Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGYHLDVSLAFSEISVGAEFNKDD 25

Db 445 LGHHGEVAKHFADLCKGAVFDADD 468

RESULT 4

US-10-403-340-15

; Sequence 15, Application US/10403340

; Publication No. US20030166565A1

; GENERAL INFORMATION:

; APPLICANT: Sims, Peter J.

; TITLE OF INVENTION: Compositions and Methods to Inhibit the

; C5b-9 Complex of Complement

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center, 1201 W. Peachtree

; St.

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/403,340

; FILING DATE: 27-Mar-2003

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/020,393B

; FILING DATE: 03-FEB-1998

; ATTORNEY/AGENT INFORMATION:

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, FILE REFERENCE: 2211R.0344
, CURRENT APPLICATION NUMBER: US/10/282,122A
, CURRENT FILING DATE: 2003-02-20
, PRIOR APPLICATION NUMBER: 60/191,078
, PRIOR FILING DATE: 2000-03-21
, PRIOR APPLICATION NUMBER: 60/206,848
, PRIOR FILING DATE: 2000-05-23
, PRIOR APPLICATION NUMBER: 60/207,727
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: 60/230,335
, PRIOR FILING DATE: 2000-09-06
, PRIOR APPLICATION NUMBER: 60/230,347
, PRIOR FILING DATE: 2000-09-09
, PRIOR APPLICATION NUMBER: 60/242,578
, PRIOR FILING DATE: 2000-10-23
, PRIOR APPLICATION NUMBER: 60/253,625
, PRIOR FILING DATE: 2000-11-27
, PRIOR APPLICATION NUMBER: 60/257,931
, PRIOR FILING DATE: 2000-12-22
, PRIOR APPLICATION NUMBER: 60/267,636
, PRIOR FILING DATE: 2001-02-09
, PRIOR APPLICATION NUMBER: 60/269,308
, PRIOR FILING DATE: 2001-02-16
, Remaining Prior Application data removed -
, NUMBER OF SEQ ID NOS: 78614
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 71303

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QY 3 GYHLDVSLAFSEISVGAEFNKD 24
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Db 210 GVSLEVQLATGNKKTGAEFNED 231

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RESULT 7
US-10-282-122A-53264
; Sequence 53264, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeelbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53264
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53264

Query Match 35.0%; Score 49; DB 15; Length 276;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 4 YHLDVSLAFSEISVGAEFNKDD 25
Db 55 FHLCERYFSNPLGIYFNEDD 76

RESULT 8
US-10-029-386-28862
; Sequence 28862, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288

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; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44593
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-44593

Query Match      34.3%; Score 48; DB 15; Length 662;
Best Local Similarity 50.0%; Pred.No. 1.3e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      8 VSLAFSEISVGAENFKDD 25
Db      127 VGFALEKTLAQNFKDD 144

RESULT 11
US-10-282-122A-75006
; Sequence 75006, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
```

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75006
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-75006

Query Match      34.3%; Score 48; DB 15; Length 666;
Best Local Similarity 50.0%; Pred.No. 1.4e+02;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      8 VSLAFSEISVGAENFKDD 25
Db      123 VGLAERTLGAQFNRPD 140

RESULT 12
US-10-282-122A-50467
; Sequence 50467, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
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; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50467
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50467

Query Match          34.3%; Score 48; DB 15; Length 690;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 8 VSLAFSEISVGAEFNKDD 25
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Db 144 VGMALGEALLAAEFNRDD 161

RESULT 13
US-09-882-694-11
; Sequence 11, Application US/09882694
; Publication No. US20030009782A1
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Crasta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; TITLE OF INVENTION: Detoxification
; FILE REFERENCE: 35718/20825
; CURRENT APPLICATION NUMBER: US/09/882,694
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1263
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 157
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-882-694-11

Query Match          34.3%; Score 48; DB 10; Length 1263;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVG 18
   ||| : ||| : |||
Db 923 CFGPHLSQSMFLAALG 940

RESULT 14
US-10-732-923-2707
; Sequence 2707, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2707
; LENGTH: 443
; TYPE: PRT

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; ORGANISM: Zea mays
US-10-732-923--2707

Query Match          33.6%; Score 47; DB 17; Length 443;
Best Local Similarity 52.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps

QY      6 LDVSLAFSEISVGAEPNKD 24
      :||| |:|:|:|
Db      110 IDVELCSDIDMGATENKD 128

RESULT 15
US-10-282-122A-71137
; Sequence 71137, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71137
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-71137

Query Match          33.6%; Score 47; DB 15; Length 662;
Best Local Similarity 36.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps

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Qy      3 GYHLDVSLAFSEISVGAEFNKD 24
         | : | : | : | : | : |
Db     120 GFAMSVGMALAEESHLACKENKD 141
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Search completed: June 8, 2005, 11:02:36
Job time : 126.767 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 12:11:59 ; Search time 22 Seconds
(without alignments)
88.222 Million cell updates/sec

Title: US-09-020-393b-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	82	2	US-08-559-492-3
2	140	100.0	557	1	Sequence 3, Appli
3	140	100.0	560	2	Sequence 16, Appl
4	140	100.0	560	2	Sequence 5, Appli
5	52	37.1	86	2	Sequence 10197, A
6	52	37.1	561	2	Sequence 4, Appli
7	48.5	34.6	417	4	Sequence 12, Appl
8	48	34.3	304	3	Sequence 20453, A
9	48	34.3	663	4	Sequence 4518, Ap
10	48	34.3	1263	3	Sequence 6441, Ap
11	48	34.3	1263	4	Sequence 11, Appl
12	48	34.3	1263	4	Sequence 11, Appl
13	48	34.3	1263	4	Sequence 11, Appl
14	47	33.6	79	4	Sequence 33666, A
15	47	33.6	79	4	Sequence 48883, A
16	46	32.9	675	3	Sequence 5219, Ap
17	45.5	32.5	611	4	Sequence 16130, A
18	45.5	32.5	658	4	Sequence 16178, A
19	45	32.1	416	4	Sequence 16172, A
20	45	32.1	542	4	Sequence 78, Appl
21	44	31.4	533	4	Sequence 20347, A
22	44	31.4	860	4	Sequence 5582, Ap
23	43.5	31.1	203	4	Sequence 45670, A
24	43	30.7	204	4	Sequence 59421, A
25	43	30.7	342	4	Sequence 44012, A
26	43	30.7	1070	4	Sequence 11321, A
27	42.5	30.4	434	4	Sequence 2222, Ap

28	42.5	30.4	440	3	US-09-134-001C-5641	Sequence 5641, Ap
29	42.5	30.4	552	4	US-09-540-236-2610	Sequence 2610, Ap
30	42.5	30.4	835	4	US-09-252-991A-32121	Sequence 32121, A
31	42	30.0	112	4	US-09-270-767-33319	Sequence 33319, A
32	42	30.0	112	4	US-09-270-767-48536	Sequence 48536, A
33	42	30.0	117	2	US-08-729-345-3	Sequence 3, Appli
34	42	30.0	132	4	US-09-270-767-61101	Sequence 61101, A
35	42	30.0	148	1	US-08-565-386-8	Sequence 8, Appli
36	42	30.0	206	3	US-09-111-311C-22	Sequence 22, Appl
37	42	30.0	238	4	US-09-583-110-3381	Sequence 3381, Ap
38	42	30.0	238	4	US-09-107-433-4307	Sequence 4307, Ap
39	42	30.0	240	4	US-09-252-991A-23766	Sequence 23766, A
40	42	30.0	270	4	US-09-902-540-13092	Sequence 13092, A
41	42	30.0	305	4	US-09-710-279-2536	Sequence 2536, Ap
42	42	30.0	359	3	US-09-347-798-12	Sequence 12, Appl
43	42	30.0	484	1	US-08-361-611-4	Sequence 4, Appli
44	42	30.0	484	1	US-08-565-655-4	Sequence 4, Appli
45	42	30.0	484	2	US-08-946-967-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-559-492-3
; Sequence 3, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-559-492-3

Query Match 100.0%; Score 140; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

Db 26 CLGYHLDVSLAFSEISVGAEFNKDDC 51

```
RESULT 2
US-08-313-288B-16
; Sequence 16, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, P-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,288B
; FILING DATE: January 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-313-288B-16

Query Match 100.0%; Score 140; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
|||
Db 378 CLGYHLDVSLAFSEISVGAEFNKDDC 403

RESULT 3
US-08-559-492-5
; Sequence 5, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMERF154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-559-492-5

Query Match 100.0%; Score 140; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
|||
Db 381 CLGYHLDVSLAFSEISVGAEFNKDDC 406

RESULT 4
US-09-949-016-10197
; Sequence 10197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10197
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10197

Query Match 100.0%; Score 140; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
|||
Db 381 CLGYHLDVSLAFSEISVGAEFNKDDC 406

RESULT 5
US-08-559-492-4
; Sequence 4, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFI54
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 85 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-559-492-4

Query Match 37.1%; Score 52; DB 2; Length 86;
Best Local Similarity 36.7%; Pred. No. 0.4;
Matches 11; Conservative 8; Mismatches 7; Indels 4; Gaps 1;

Qy 1 CLGYHLDVSLAF-----SEISVGAEFNKDDC 26
Db 26 CLGFDDLNLNIPGKSAGLSLTGQANKNC 55

RESULT 6
US-08-559-492-12
; Sequence 12, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFI54
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
```

```
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-559-492-12

Query Match 37.1%; Score 52; DB 2; Length 561;
Best Local Similarity 36.7%; Pred. No. 4.5;
Matches 11; Conservative 8; Mismatches 7; Indels 4; Gaps 1;

Qy 1 CLGYHLDVSLAF-----SEISVGAEFNKDDC 26
Db 389 CLGFDDLNLNIPGKSAGLSLTGQANKNC 418

RESULT 7
US-09-252-991A-20453
; Sequence 20453, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20453
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20453

Query Match 34.6%; Score 48.5; DB 4; Length 417;
Best Local Similarity 35.3%; Pred. No. 12;
Matches 12; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

Qy 2 LGYHLDVSLAFSEISVGAEFN-----KDDC 26
Db 153 LTPVLSVVRFSETPVGAEYSMARAAAGRGDEC 186

RESULT 8
US-09-134-001C-4518
; Sequence 4518, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4518
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-4518

Query Match 34.3%; Score 48; DB 3; Length 304;
Best Local Similarity 36.0%; Pred. No. 9.4;
```


RESULT 13

US-09-882-694B-11
; Sequence 11, Application US/09882694B
; Patent No. 6822140
; GENERAL INFORMATION:
; APPLICANT: DuVick, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Crasta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; FILE REFERENCE: 35718/208255
; CURRENT APPLICATION NUMBER: US/09/882,694B
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1263
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa is any amino acid

US-09-882-694B-11

Query Match 34.3%; Score 48; DB 4; Length 1263;
Best Local Similarity 44.4%; Pred. No. 59;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CLGYHLDVSLAFSEISVG 18
| | | | | : | | | | : | |
Db 923 CFGFHLQSMEFLAIALG 940

RESULT 14

US-09-270-767-33666
; Sequence 33666, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33666
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-33666

Query Match 33.6%; Score 47; DB 4; Length 79;
Best Local Similarity 40.0%; Pred. No. 2.5;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 DVSLAFSEISVGAEFNKDDC 26
: : | | : : | | : : | |
Db 6 NIHLISSQLCVGGGEFYRDSC 25

RESULT 15

US-09-270-767-48883
; Sequence 48883, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48883
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-48883

Query Match 33.6%; Score 47; DB 4; Length 79;
Best Local Similarity 40.0%; Pred. No. 2.5;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 DVSLAFSEISVGAEFNKDDC 26
: : | | : : | | : : | |
Db 6 NIHLISSQLCVGGGEFYRDSC 25

Search completed: June 8, 2005, 12:12:28
Job time : 22 secs

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:17:55 ; Search time 38 Seconds
(without alignments)
65.833 Million cell u

Title: US-09-020-393B-14 COPY 26 51

Perfect score: 140
Sequence: 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs. 96216763 residues

Total number of hits satisfying chosen parameters: 5210

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Minimum DB seq length: 0
Maximum DB seq length: 26
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

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1:  _pir1:*
2:  _pir2:*
3:  _pir3:*
4:  _pir4:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	22.1	22	2	T25653	hypothetical prote
2	28	20.0	17	2	A60889	olfactory glycopro
3	28	20.0	22	2	A83199	C-type natriuretic
4	27	19.3	22	2	JP0066	ribosomal protein
5	27	19.3	25	2	S7574	malate dehydrogena
6	26.5	18.9	20	2	S72501	protein kinase C I
7	26	18.6	15	2	S08301	epidermal growth f
8	26	18.6	18	2	A61392	brain-associated s
9	26	18.6	21	2	I65370	collagen alpha 1(I
10	26	18.6	24	1	B32252	pyrroloquinoline q
11	26	18.6	24	2	T46622	hypothetical prote
12	26	18.6	25	2	A48810	fibrinogen B beta
13	25	17.9	20	2	A60295	apolipoprotein III
14	24	17.1	17	2	S71864	glutathione transf
15	24	17.1	17	2	A36727	cytochrome c551 -
16	24	17.1	21	2	S38739	lipid transfer pro
17	24	17.1	22	2	C46285	formaldehyde dehyd
18	24	17.1	22	2	PC2134	maltose transport
19	24	17.1	23	2	S38738	lipid transfer pro
20	23	16.4	14	2	PS0371	hypothetical prote
21	23	16.4	14	2	B61597	cytochrome P450 AL
22	23	16.4	15	2	D56385	nitrophenol 4 - Rh
23	23	16.4	15	2	A47628	Fc gamma receptor
24	23	16.4	15	2	PA0062	fumarate hydratase
25	23	16.4	16	2	B45895	T-cell surface gly
26	23	16.4	17	2	PH1357	Ig heavy chain D μ
27	23	16.4	18	2	S36121	lectin - spurge (E
28	23	16.4	19	2	A38386	Ca2+-transporting
29	23	16.4	22	2	JT0581	natriuretic peptid

ALIGNMENTS

RESULT 1

T25853
hypothetical protein C47C12.5 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
C/Accession: T25653
R/Connell, M.
submitted to the EMBL Data Library, August 1996
A/Description: The sequence of *C. elegans* cosmid C47C12.5
A/Reference number: Z20062
A/Accession: T25653
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-22 <CON>
A/Cross-references: EMBL:U67951; PIDD:AA807573.1; GSPDB:
A/Experimental source: strain Bristol N2; clone C47C12
C/Genetics:
A/Gene: CESP:C47C12.5
A/Map position: X
A/Introns: 21/1

Query Match 22.1%; Score 31; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 9: Conservative 2: Mismatches 5: Indels

Qy 5 HLDV--SLAFSEISVGAE 20
| | : | | | | : |
Db 4 HSDIGNSLOPFRISLKNE 21

RESULT 2

A60889
Olfactory glycoprotein RB-8 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60889
R:Schwob, J.E.; Gottlieb, D.I.
J. Neurosci. 8, 3470-3480, 1988
A:Title: Purification and characterization of an antigen that is spatially
A:Reference number: A60889; MUID:89010968; PMID:3171695

Query Match 20.0%; Score 28; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 6.5e+02;
Matches 6: Conservative 3: Mismatches 2: Indels

Qv 8 VSLAFSEISVG 18

brain natriuretic
pyroglutamine q
cytochrome-c oxidase
CDK inhibitor - mo
gamma-glutamyl tra
annexin v - rat (f
probable photosyst
buccalin - Califor
cartilage oligomer
conserved hypothet
major milk gland p
outer layer protei
hypothetical prote
pyroglutamine q
DNA-binding protei
glutathione transf

```
Db          6 ISLSKVELSVG 16
          :||: ||||
          :||: ||||

RESULT 3
A36399
C-type natriuretic peptide - frog
C;Species: Ranidae gen. sp. (frog)
C;Date: 01-Feb-1991 #sequence_revision 01-Feb-1991 #text_change 09-Jul-2004
C;Accession: A36399
R;Yoshihara, A.; Kozawa, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 173, 591-598, 1990
A;Title: Isolation and sequence determination of frog C-type natriuretic peptide.
A;Reference number: A36399; MUID:91083642; PMID:2148082
A;Accession: A36399
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <Y0S>
A;Cross-references: UNIPROT:P20968
C;Superfamily: natriuretic peptide A precursor

Query Match      20.0%; Score 28; DB 2; Length 22;
Best Local Similarity 53.8%; Pred. No. 8.6e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CLGYHLDSVLAIFS 13
      |||||
Db 6 CFGVLDRIQAFS 18

RESULT 4
JP0066
ribosomal protein L30 - Nocardia asteroides (fragment)
C;Species: Nocardia asteroides
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: JP0066
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p
A;Reference number: JP0042
A;Accession: JP0066
A;Molecule type: protein
A;Residues: 1-22 <OCH>
A;Cross-references: UNIPROT:Q7M028
C;Keywords: protein biosynthesis; ribosome

Query Match      19.3%; Score 27; DB 2; Length 22;
Best Local Similarity 26.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 7 DVSLAFSEISVGAEFNKDD 25
      | : : : ||| : |
Db 2 DLKVQIKSTIGAKANQKD 20

RESULT 5
S07574
malate dehydrogenase (EC 1.1.1.37) - Phenylbacterium immobile (fragment)
C;Species: Phenylbacterium immobile
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S07574
R;Rommel, T.O.; Hund, H.K.; Speth, A.R.; Lingens, F.
Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A;Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydrogen
A;Reference number: S04956; MUID:89374824; PMID:2775496
A;Accession: S07574
A;Molecule type: protein
A;Residues: 1-25 <ROW>
A;Cross-references: UNIPROT:P19980
C;Superfamily: L-lactate dehydrogenase
C;Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match      19.3%; Score 27; DB 2; Length 25;
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```
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGVHL 6
      :|||
Db 16 IGYHL 20

RESULT 6
S72501
protein kinase C inhibitor - human (fragment)
N;Alternate names: histidine triad nucleotide-binding protein
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S72501; S62623
R;Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A;Title: Purification and characterization of human biliverdin reductase.
A;Reference number: S29736; MUID:93143333; PMID:8424666
A;Accession: S72501
A;Molecule type: protein
A;Residues: 1-20 <MAI>
A;Note: this protein was identified as biliverdin reductase; the identification is quest
R;Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A;Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization
A;Reference number: S62622; MUID:96202961; PMID:8631357
A;Accession: S62623
A;Molecule type: protein
A;Residues: 1-20 <MAW>
A;Superfamily: protein kinase C inhibitor; histidine triad homology
C;Keywords: homodimer; protein kinase inhibitor; zinc

Query Match      18.9%; Score 26.5; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CLGYHLDSVS 9
      || : || : |
Db 1 CLAFH-DIS 8

RESULT 7
S08301
epidermal growth factor, high molecular weight - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S08301
R;Nexo, E.; Jorgensen, P.E.; Thim, L.; Roepstorff, P.
Biochim. Biophys. Acta 1037, 388-393, 1990
A;Title: Purification and characterization of a low and a high molecular weight form of
A;Reference number: S08288; MUID:90181442; PMID:2310752
A;Accession: S08301
A;Molecule type: protein
A;Residues: 1-15 <NEX>
A;Cross-references: UNIPROT:Q7M0D2
C;Keywords: growth factor

Query Match      18.6%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDDC 26
      ||||
Db 3 KDDC 6

RESULT 8
A61392
brain-associated small cell lung cancer antigen - human (fragment)
N;Alternate names: BASCA
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
```

C;Accession: A61392
R;Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A;Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1
A;Reference number: A61392; MUID:92046737; PMID:1719260
A;Accession: A61392
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <UME>

Query Match 18.6%; Score 26; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 LDVSLAFSEISVG 18
: : : : :
Db 3 VDVPVSGEISVG 15

RESULT 9
I65270
collagen alpha 1(I) chain - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I65270
R;Genovese, C.; Rowe, D.; Kream, B.
Biochemistry 23, 6210-6216, 1984
A;Title: Construction of DNA sequences complementary to rat alpha-1 and alpha-2 collagen
A;Reference number: I52392; MUID:85122694; PMID:6395893
A;Accession: I65270
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-21 <RES>
A;Cross-references: UNIPROT:Q63076; GB:M12200; NID:G203191; PIDN:AAA40835.1; PID:G203195
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 18.6%; Score 26; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 YHLDVSLAFSEISVG 18
: : : : :
Db 7 YHCKNSIAYLDEERG 21

RESULT 10
B32252
pyrroloquinoline quinone precursor - Acinetobacter calcoaceticus
N;Alternate names: pqg gene IV protein
C;Species: Acinetobacter calcoaceticus
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: B32252
R;Goosen, N.; Horsman, H.P.A.; Huinen, R.G.M.; van de Putte, P.
J. Bacteriol. 171, 447-455, 1989
A;Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyrro
A;Reference number: A32252; MUID:89123056; PMID:2536663
A;Accession: B32252
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-24 <GOO>
A;Cross-references: UNIPROT:P27532; GB:X06452; NID:G38740; PID:gl30796
R;Goosen, N.; Huinen, R.G.; van de Putte, P.
J. Bacteriol. 174, 1426-1427, 1992
A;Title: A 24-amino-acid polypeptide is essential for the biosynthesis of the coenzyme p
A;Reference number: A59183; MUID:92138642; PMID:1310505
A;Contents: annotation
C;Genetics:
A;Gene: pqga
C;Superfamily: pyrroloquinoline quinone precursor pqga
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 18.6%; Score 26; DB 1; Length 24;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 11 AFSEISVGAE 20
: : : : :
Db 7 AFTDLRIGFE 16

RESULT 11
T46622
hypothetical protein c1 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46622
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A;Reference number: Z23105
A;Accession: T46622
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-24 <CHA>
A;Cross-references: EMBL:U31309; NID:G974285; PID:G974287
A;Experimental source: strain 56PT2xs6PT3; 8 month seedlings

Query Match 18.6%; Score 26; DB 2; Length 24;
Best Local Similarity 41.7%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAF 12
: : : : :
Db 11 CQGFQPCILCF 22

RESULT 12
A48810
fibrinogen B beta subunit - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48810
R;Roberts, L.R.; Nichols, L.A.; Holland, L.J.
Biochemistry 32, 11627-11637, 1993
A;Title: transcriptional regulation of the Xenopus laevis B beta fibrinogen subunit gene
A;Reference number: A48810; MUID:94032285; PMID:8218230
A;Accession: A48810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <ROB>
A;Cross-references: UNIPROT:Q91589; GB:U05035; GB:S66373; NID:G450950; PIDN:AAA60463.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:138880, NCBIP:138881)

Query Match 18.6%; Score 26; DB 2; Length 25;
Best Local Similarity 23.5%; Pred. No. 2e+03;
Matches 4; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 9 SLAFSEISVGAEFNKDD 25
: : : : :
Db 8 ALCVSAVWCSSDYDEDD 24

RESULT 13
A60295
apolipophorin III - house cricket (fragment)
C;Species: Acheta domestica (house cricket)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60295
R;Strobel, L.M.; Kanost, M.R.; Ziegler, R.; Wells, M.A.
Insect Biochem. 20, 859-863, 1990
A;Title: Adipokinetic hormone causes formation of a low density lipophorin in the house
A;Reference number: A60295
A;Accession: A60295

```

A;Molecule type: protein
A;Residues: 1-20 <STR>
A;Cross-references: UNIPROT:Q7M484
C;Comment: This protein, a small, water-soluble apolipoprotein, is thought to increase the rate of lipid transport.
C;Keywords: hemolymph; lipid transport

Query Match      17.9%; Score 25; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 16 SVGAEN 22      :|||
Db 4 TTGADFN 10

RESULT 14
S71864
Glutathione transferase (EC 2.5.1.18) class alpha 6a - pig (fragment)
N;Alternate names: glutathione S-transferase class alpha 6a
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71864
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrophoresis
A;Reference number: S71864; MUID:96332484; PMID:8760377
A;Accession: S71864
A;Molecule type: protein
A;Residues: 1-17 <ROU>
A;Cross-references: UNIPROT:Q7M3E7
A;Experimental source: liver; cytosolic
C;Comment: At least five species-independent classes of cytosolic glutathione transferases have been identified in various tissues.
C;Complex: dimer
C;Function:
A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a variety of substrates
A;Pathway: detoxification; xenobiotics metabolism
A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
C;Superfamily: glutathione transferase
C;Keywords: dimer; transferase

Query Match      17.1%; Score 24; DB 2; Length 17;
Best Local Similarity 35.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 DVSLAFSEISVGAE 20
Db 1 DGSLLFQQVDVMTYE 14

RESULT 15
A36727
cytochrome c551 - Methylobionas sp. (fragment)
C;Species: Methylobionas sp.
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36727
R;DiSpirito, A.A.; Lipscomb, J.D.; Lidstrom, M.E.
J. Bacteriol. 172, 5360-5367, 1990
A;Title: Soluble cytochromes from the marine methanotroph Methylobionas sp. strain A4.
A;Reference number: A36727; MUID:90368596; PMID:2168380
A;Accession: A36727
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <DIS>
A;Cross-references: UNIPROT:Q7M0P4

Query Match      17.1%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLGYH 5

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:09:50 ; Search time 166 Seconds
(without alignments)
80.205 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CIGYHLDVSLAFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 18167

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	24.3	26	1 PQQA_GLUOX	Q913B4 gluconobact
2	34	24.3	26	2 Q8VL82	Q8VL82 staphylococ
3	31	22.1	19	2 Q9TWH2	Q9TWH2 oxytricha g
4	30	21.4	23	2 Q7RR84	Q7RR84 plasmodium
5	30	21.4	24	2 Q7PIC4	Q7PIC4 anopheles g
6	30	21.4	26	2 Q41052	Q41052 porphyra sp
7	28	20.0	15	2 Q9R569	Q9R569 nitrosomona
8	28	20.0	19	2 Q9TWK8	Q9TWK8 trypanosoma
9	28	20.0	20	2 Q7ZGQ9	Q7ZGQ9 human t-cel
10	28	20.0	21	2 Q82392	Q82392 human t-cel
11	28	20.0	21	2 Q82410	Q82410 human t-cel
12	28	20.0	21	2 Q82411	Q82411 human t-cel
13	28	20.0	21	2 Q82412	Q82412 human t-cel
14	27	19.3	15	2 Q9UC67	Q9UC67 homo sapien
15	27	19.3	20	2 Q9TRA4	Q9TRA4 sus scrofa
16	27	19.3	22	2 Q7M028	Q7M028 nocardia as
17	27	19.3	25	1 GLP1_CITSI	P84159 citrus sine
18	27	19.3	25	1 MDH_EHEIM	P19980 phenyllobact
19	26.5	18.9	26	2 Q8JDU8	Q8JDU8 human immun
20	26.5	18.9	26	2 Q8JDK2	Q8JDK2 human immun
21	26.5	18.9	26	2 Q8JDK6	Q8JDK6 human immun
22	26	18.6	14	2 Q71GU0	Q71GU0 andrena ili
23	26	18.6	14	2 Q71GS8	Q71GS8 andrena aff
24	26	18.6	14	2 Q71G26	Q71G26 andrena kri
25	26	18.6	14	2 Q71H10	Q71H10 andrena hel
26	26	18.6	14	2 Q71H20	Q71H20 andrena dis
27	26	18.6	14	2 Q71H46	Q71H46 andrena ali
28	26	18.6	15	2 Q7MOD2	Q7MOD2 rattus norv
29	26	18.6	20	2 Q3DE23	Q3DE23 gallus gall
30	26	18.6	21	2 Q63076	Q63076 rattus norv
31	26	18.6	22	2 Q9ZZ72	Q9ZZ72 phlebotomus

32	26	18.6	22	2	Q9ZZ74	Q9ZZ74 phlebotomus
33	26	18.6	23	2	Q7RDX8	Q7RDX8 plasmodium
34	26	18.6	24	1	PQQA_ACICA	P27532 acinetobact
35	26	18.6	25	2	Q788Y7	Q788Y7 xenopus lae
36	25	17.9	13	2	Q92820	Q92820 chimpanzee
37	25	17.9	16	2	Q9R5S7	Q9R5S7 treponema d
38	25	17.9	20	1	TPX_CLOPA	P81361 clostridium
39	25	17.9	20	2	Q8T3M3	Q8T3M3 drosophila
40	25	17.9	20	2	Q7M484	Q7M484 acheta dome
41	25	17.9	23	2	Q6F9J3	Q6F9J3 acinetobact
42	25	17.9	24	2	Q819U5	Q819U5 periplaneta
43	25	17.9	24	2	Q7RLJ2	Q7RLJ2 plasmodium
44	25	17.9	24	2	Q61946	Q61946 mus musculu
45	25	17.9	25	2	Q26089	Q26089 polycelis n

ALIGNMENTS

RESULT 1

PQQA_GLUOX	STANDARD;	PRT;	26 AA.
ID PQQA_GLUOX			
AC Q9L3B4;			
DT 10-OCT-2003 (Rel. 42, Created)			
DT 10-OCT-2003 (Rel. 42, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DE Coenzyme PQQ synthesis protein A (Pyroloquinoline quinone			
DE biosynthesis protein A).			
GN Name=pqqa;			
OS Gluconobacter oxydans (Gluconobacter suboxydans).			
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;			
OC Acetobacteraceae; Gluconobacter.			
OX NCBI_TaxID=442;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 9937;			
RX MEDLINE=20564161; PubMed=11111029;			
RA Felder M., Gupta A., Verma V., Kumar A., Qazi G.N., Cullum J.;			
RT "The pyrroloquinoline quinone synthesis genes of Gluconobacter			
RT oxydans.";			
RL FEMS Microbiol. Lett. 193:231-236(2000).			
CC - - FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)			
CC biosynthesis. Probably provides the glutamate and tyrosine			
CC residues that are cross-linked and modified to form the coenzyme			
CC - - PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.			
CC - - SIMILARITY: Belongs to the pqqa family.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC use by non-profit institutions as long as its content is in no way			
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CC or send an email to license@isb-sib.ch).			
CC -----			
CC EMBL; AJ277117; CAB83197.1; -			
DR HAMAP; MF 00656; -; 1.			
KW PQQ: PQQ biosynthesis.			
FT CROSSLINK 16 20			
FT Pyroloquinoline quinone (Glu-Tyr)			
FT (Probable).			
SQ SEQUENCE 26 AA; 2879 MW; 22131FCE0D70987D CRC64;			

Query Match 24.3%; Score 34; DB 1; Length 26;

Best Local Similarity 50.0%; Pred. No. 8.2e+02;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNKDDC 26

Db 9 TEIPLGAEINSYVC 22

RESULT 2

```

Q8VL82
ID Q8VL82 PRELIMINARY; PRT; 26 AA.
AC Q8VL82;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCS1978, and JCS1968;
RX MEDLINE=21482917; PubMed=11597450; DOI=10.1016/S0966-842X(01)02175-8;
RA Hiramatsu K., Cui L., Kuroda M., Ito T.;
RT "The emergence and evolution of methicillin-resistant Staphylococcus aureus.";
RL Trends Microbiol. 9:486-493 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JCS1978, and JCS1968;
RX MEDLINE=21895198; PubMed=11897611;
RA Ma X.X., Ito T., Tienasatorn C., Jamklang M., Chongtrakool P.,
RA Boyle-Vavra S., Daum R.S., Hiramatsu K.;
RT "Novel type of staphylococcal cassette chromosome mec identified in community-acquired methicillin-resistant Staphylococcus aureus strains.";
RL Antimicrob. Agents Chemother. 46:1147-1152 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=JCS1978, and JCS1968;
RA Ito T., Okuma K., Xue M.X., Yuzawa H., Hiramatsu K.;
RT "Insights on antibiotic resistance of Staphylococcus aureus from its whole genome: genomic island SCC.";
RL Drug Resist. Updat. 6:41-52 (2003).
DR EMBL; AB063173; BAB72134.1; -.
DR EMBL; AB063172; BAB72115.1; -.
KW Hypothetical protein.
SQ SEQUENCE 26 AA; 3114 MW; B93553ACB62BBB8A8 CRC64;

Query Match 24.3%; Score 34; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 8.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CLGYHLDVSLAF 12
Db 14 CLNRKLEVSITP 25

RESULT 3
Q9TWH2
ID Q9TWH2 PRELIMINARY; PRT; 19 AA.
AC Q9TWH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE H protein (fragment).
OS Oxytricha granulifera.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Oxytricha.
OX NCBI_TaxID=5947;
RN [1]
RP SEQUENCE.
RX MEDLINE=95345843; PubMed=7620461;
RA Irato P., Piccini E., James P., Ammermann D.;
RT "Evidence of a cadmium-thionein and the glycine cleavage system in Oxytricha granulifera.";
RL J. Eukaryot. Microbiol. 42:376-378 (1995).
SQ SEQUENCE 19 AA; 2381 MW; 4C0B5E62B50A0984 CRC64;

Query Match 22.1%; Score 31; DB 2; Length 19;
Best Local Similarity 46.2%; Pred. No. 1.8e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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```

QY 12 FSEISVGAEFNKD 24
Db 5 FTEDAWEVYKND 17

RESULT 4
Q7RR84
ID Q7RR84 PRELIMINARY; PRT; 23 AA.
AC Q7RR84;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (fragment).
GN Name=PY00850;
OS Plasmodium Yoelii Yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AABL0100029; EAA18932.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2809 MW; 9DA5AE1C1AB7333E CRC64;

Query Match 21.4%; Score 30; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 3.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYHLDV 8
Db 8 GFHLDI 13

RESULT 5
Q7PIC4
ID Q7PIC4 PRELIMINARY; PRT; 24 AA.
AC Q7PIC4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000023104 (fragment).
GN Name=ENSANGG0000021148;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC

```

DR EMBL; AAB01008960; EAA44199.1; --
FT NON_TER 1 1
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2889 MW; 7449585CEBDB1AC4B CRC64;

Query Match 21.4%; Score 30; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLGYHL 6
|:|:|:
Db 4 CSGYHI 9

RESULT 6

ID Q41052 PRELIMINARY; PRT; 26 AA.
AC Q41052;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Var. amplifolia DNA sequence with partial cds. (Fragment).
OS Porphyra spiralis.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.
OX NCBI_TaxID=31350;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PSA-B/Upatuba;
RX MEDLINE=94224117; PubMed=8170361;
RA Oliveira M.C., Ragan M.A.;
RT "Variant forms of a Group I intron in nuclear small-subunit rRNA genes of the marine red alga Porphyra spiralis var. amplifolia";
RL Mol. Biol. Evol. 11:195-207(1994).
DR EMBL; L26175; AAA72417.1; --
FT NON_TER 26 26
SQ SEQUENCE 26 AA; 2821 MW; 9F53369E65A2254F CRC64;

Query Match 21.4%; Score 30; DB 2; Length 26;
Best Local Similarity 40.8%; Pred. No. 3.5e+03;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YHLDVSLAFSEISVG 18
|:|:|:
Db 5 YHLEGEVTRFSVG 19

RESULT 7

ID Q9R569 PRELIMINARY; PRT; 15 AA.
AC Q9R569;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hydroxylamine oxidoreductase (Fragment).
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE.
RX MEDLINE=93315429; PubMed=8325841;
RA Arciero D.M., Hooper A.B.;
RT "Hydroxylamine oxidoreductase from Nitrosomonas europaea is a multimer of an octa-heme subunit";
RL J. Biol. Chem. 268:14645-14654(1993).
DR InterPro; IPR000345; CytoC heme BS.
DR PROSITE; PS00190; CYTOCHROME_C7; UNKNOWN 1.
SQ SEQUENCE 15 AA; 1687 MW; 983D4B8A13698849 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 4.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLGYHLDVS 9
|:|:|:
Db 5 CIDCHVDVN 13

RESULT 8

Q9TWK8 PRELIMINARY; PRT; 19 AA.
ID Q9TWK8
AC Q9TWK8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Haptoglobin-related protein beta subunit (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=95232503; PubMed=7716520;
RA Smith A.B., Esko J.D., Hajduk S.L.;
RT "Killing of trypanosomes by the human haptoglobin-related protein.";
RL Science 268:284-286(1995).
SQ SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 19;
Best Local Similarity 54.5%; Pred. No. 5.3e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LGYHLDVSLAF 12
|:|:|:
Db 2 LGGHLDKAGSF 12

RESULT 9

Q7ZGQ9 PRELIMINARY; PRT; 20 AA.
ID Q7ZGQ9
AC Q7ZGQ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tax protein (Fragment).
GN Name=tax;
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94047388; PubMed=8230487;
RA Pardi D., Kaplan J.E., Coligan J.E., Folks T.M., Lal R.B.;
RT "Identification and characterization of an extended Tax protein in human T-cell lymphotropic virus type II subtype b isolates.";
RL J. Virol. 67:7663-7667(1993).
DR EMBL; S66926; AAP13991.1; --
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2254 MW; 11F39408273646D0 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 20;
Best Local Similarity 35.7%; Pred. No. 5.6e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 FSEISVGAEFNKDD 25
|:|:|:
Db 1 YTNIPVSILFNKEE 14

RESULT 10

Q82392 PRELIMINARY; PRT; 21 AA.
ID Q82392
AC Q82392;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).

```
GN Name-tax;
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroviral viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190544; PubMed=8627666;
RA Eiraku N., Novoa P., Monken C., Oliveira M.D., Oliveira O.D.,
RA Ishak R., Oliveira M.P., Laureiro P., Ishak M., Acevedo V.,
RA Hammershlag N., Zhu S.W., Kubo T., Hall W.W.;
RT "Identification and characterization of a new and distinct molecular
RT subtype of human T-cell lymphotropic virus type 2.";
RL J. Virol. 70:1481-1492(1996).
DR EMBL; U32871; AAB04905.1; -.
FT NON TER 1
SQ SEQUENCE 21 AA; 2383 MW; 11F39408575CF6D0 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.9e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 FSEISVGAEFNKDD 25
Db 2 YTNIPVSILFNKEE 15

RESULT 11
Q82410 PRELIMINARY; PRT; 21 AA.
AC Q82410;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).
GN Name-tax;
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroviral viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190544; PubMed=8627666;
RA Eiraku N., Novoa P., Monken C., Oliveira M.D., Oliveira O.D.,
RA Ishak R., Oliveira M.P., Laureiro P., Ishak M., Acevedo V.,
RA Hammershlag N., Zhu S.W., Kubo T., Hall W.W.;
RT "Identification and characterization of a new and distinct molecular
RT subtype of human T-cell lymphotropic virus type 2.";
RL J. Virol. 70:1481-1492(1996).
DR EMBL; U32883; AAB04923.1; -.
FT NON TER 1
SQ SEQUENCE 21 AA; 2383 MW; 11F39408575CF6D0 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.9e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 FSEISVGAEFNKDD 25
Db 2 YTNIPVSILFNKEE 15

RESULT 12
Q82411 PRELIMINARY; PRT; 21 AA.
AC Q82411;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).
GN Name-tax;
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroviral viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=96190544; PubMed=8627666;
RA Eiraku N., Novoa P., Monken C., Oliveira M.D., Oliveira O.D.,
RA Ishak R., Oliveira M.P., Laureiro P., Ishak M., Acevedo V.,
RA Hammershlag N., Zhu S.W., Kubo T., Hall W.W.;
RT "Identification and characterization of a new and distinct molecular
RT subtype of human T-cell lymphotropic virus type 2.";
RL J. Virol. 70:1481-1492(1996).
DR EMBL; U32884; AAB04924.1; -.
FT NON TER 1
SQ SEQUENCE 21 AA; 2383 MW; 11F39408575CF6D0 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.9e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 FSEISVGAEFNKDD 25
Db 2 YTNIPVSILFNKEE 15

RESULT 13
Q82412 PRELIMINARY; PRT; 21 AA.
AC Q82412;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).
GN Name-tax;
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroviral viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190544; PubMed=8627666;
RA Eiraku N., Novoa P., Monken C., Oliveira M.D., Oliveira O.D.,
RA Ishak R., Oliveira M.P., Laureiro P., Ishak M., Acevedo V.,
RA Hammershlag N., Zhu S.W., Kubo T., Hall W.W.;
RT "Identification and characterization of a new and distinct molecular
RT subtype of human T-cell lymphotropic virus type 2.";
RL J. Virol. 70:1481-1492(1996).
DR EMBL; U32885; AAB04925.1; -.
FT NON TER 1
SQ SEQUENCE 21 AA; 2383 MW; 11F39408575CF6D0 CRC64;

Query Match 20.0%; Score 28; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.9e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 FSEISVGAEFNKDD 25
Db 2 YTNIPVSILFNKEE 15

RESULT 14
Q9UC67 PRELIMINARY; PRT; 15 AA.
AC Q9UC67;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 40.2 kDa haptoglobin beta-chain homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95364343; PubMed=7637327;
RA Kliffen M., de Jong P.T., Luider T.M.;
RT "Protein analysis of human maculae in relation to age-related
RT maculopathy.";
```

```
RL Lab. Invest. 73:267-272(1995).
SQ SEQUENCE 15 AA; 1649 MW; D7C94056162D5510 CRC64;

Query Match 19.3%; Score 27; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 6.1e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 LGVHLDVSLAP 12
   |||||
Db 2 LGGHLDAKGF 12

RESULT 15
Q9TRA4 PRELIMINARY; PRT; 20 AA.
AC Q9TRA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE PAMP=PROADRENOMEDULLIN N-terminal 20 peptide (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=94357274; PubMed=8076689; DOI=10.1016/0014-5793(94)00810-8;
RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT "Identification and hypotensive activity of proadrenomedullin N-
RT terminal 20 peptide (PAMP).";
RL FEBS Lett. 351:35-37(1994).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2446 MW; 9604950BAF426114 CRC64;

Query Match 19.3%; Score 27; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 13 SEISVGAEFNK 23
   : |||||
Db 1 ARLDVAAEPRK 11

Search completed: June 8, 2005, 11:26:56
Job time : 169 secs
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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:08:59 ; Search time 157 Seconds
(without alignments)
64.049 Million cell updates/sec

Title: US-09-020-393b-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAFSEISVGRFKNKDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 776640

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: Genesep16Dec04:*
2: Genesep1980s:*
3: Genesep1990s:*
4: Genesep2000s:*
5: Genesep2001s:*
6: Genesep2002s:*
7: Genesep2003as:*
8: Genesep2003bs:*
9: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	25.0	15	3	AAY77161
2	35	25.0	15	7	ADL16019
3	35	25.0	15	8	ADJ56718
4	34.5	24.6	23	6	ADBI6907
5	34	24.3	19	4	AAE00613
6	34	24.3	19	8	ADO16864
7	34	24.3	20	2	AAW35697
8	34	24.3	20	5	AAU77896
9	34	24.3	20	8	ADK14728
10	34	24.3	21	2	AAW82186
11	34	24.3	21	4	AAG73204
12	34	24.3	21	4	AAG73203
13	34	24.3	21	8	ADN88519
14	34	24.3	21	8	ADN88443
15	34	24.3	26	3	AAV96324
16	34	24.3	26	4	AAAB70374
17	33.5	23.9	25	5	ADH32596
18	33	23.6	12	5	ABB08996
19	33	23.6	12	5	AAE16656
20	33	23.6	12	5	AAU74830
21	33	23.6	12	5	ABB07591
22	33	23.6	12	6	ABP97968
23	33	23.6	12	6	AAO26794
24	33	23.6	12	7	ADC9716
25	33	23.6	12	7	ADD80762

26	33	23.6	12	8	ADI64642
27	33	23.6	12	8	ADP45538
28	33	23.6	13	4	ABB55917
29	33	23.6	13	4	ABB55868
30	33	23.6	13	4	ABB55986
31	33	23.6	13	4	AAU28555
32	33	23.6	13	4	AAU24984
33	33	23.6	13	4	AAU24994
34	33	23.6	13	4	AAU26202
35	33	23.6	13	4	AAU15328
36	33	23.6	13	4	AAU15338
37	33	23.6	13	4	ABB52344
38	33	23.6	13	4	ABB52357
39	33	23.6	13	5	ABB06591
40	33	23.6	13	5	ABG78526
41	33	23.6	13	6	ABP57217
42	33	23.6	13	6	ABR59132
43	33	23.6	13	8	ADN32024
44	33	23.6	13	8	ADO78595
45	33	23.6	13	8	ADO78605

ALIGNMENTS

RESULT 1
AAY77161
ID AAY77161 standard; peptide; 15 AA.
XX
AC AAY77161;
XX
DT 08-MAY-2000 (first entry)
XX
DE FGFR-binding peptide 13-1, SEQ ID NO:23.
XX
KW Fibroblast growth factor receptor; FGFR ligand; activation;
KW phage display library; agonist; antagonist; drug screening;
KW competitive inhibitor; angiogenic; wound healing.
XX
OS Synthetic.
XX
PN WO200003245-A1.
XX
PD 20-JAN-2000.
XX
PF 28-MAY-1999; 99WO-US011844.
XX
PR 28-MAY-1998; 98US-0087107P.
XX
PA (CHUS) CHUGAI PHARM CO LTD.
XX
PI McConnell SJ, Spinella DG;
XX
DR WPI; 2000-160963/14.
XX
N-PSDB; AA287257.
XX
PT New polypeptide useful as a receptor agonist or antagonist in treating
PT wounds and promoting angiogenic capability, and as a model for designing
PT small molecules with agonist or antagonist activity.
XX
PS Claim 16; Page 65; 83pp; English.
XX
CC Sequences AAY77154-Y77174 represent novel peptides capable of binding to
CC and activating human fibroblast growth factor receptor (FGFR). The
CC peptides of the invention have amino acid sequences that are unrelated to
CC that of the human FGFR or to those of prior art FGFR-binding peptides.
CC The peptides were isolated from phage display libraries via their ability
CC to bind an FGFR probe. Peptide 13-1 (AAY77161) was used as the basis for
CC the construction of an evolved phage display library, which led to the
CC identification of further peptides (AAY77168-Y77174, consensus sequence
CC AAY77153) capable of binding human FGFR. The peptides (or peptide
CC mimetics) can be used to activate human FGFR, or can be used as
CC competitive inhibitors to inhibit the binding of FGF to its receptor. The

CC invention also encompasses methods of screening drugs that mimic human
CC FGF. The peptides are useful as FGF agonist or antagonist therapeutic
CC agents for treating wounds and promoting angiogenesis. The peptides are
CC also useful as a model for designing small molecules which have FGF
CC agonist or antagonist activity. The peptides are stable and economical,
CC and are alternatives to expensive recombinant FGF or FGF isolated from
CC animal tissue. In addition, they have an improved therapeutic delivery
CC effect and pharmacokinetics
XX
SQ Sequence 15 AA;

Query Match 25.0%; Score 35; DB 3; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 13 SEISVGAEFNKDDC 26
| : ||| | : ||
Db 2 SALFVGAPFHVPDC 15

RESULT 2
ADL16019
ID ADL16019 standard; peptide; 15 AA.
XX
AC ADL16019;
XX
DT 06-MAY-2004 (first entry)
XX
DE Fibroblast growth factor peptide ligand.
XX
KW solid phase synthesis; peptide-spacer-lipid conjugate; targeted liposome;
KW cytotstatic; somatostatin receptor 2 inhibitor;
KW somatostatin receptor expressed cancer; cancer.
XX
OS Synthetic.
XX
PN EP1319667-A2.
XX
PD 18-JUN-2003.
XX
PF 09-DEC-2002; 2002EP-00258470.
XX
PR 07-DEC-2001; 2001US-00016569.
XX
PA (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI Wu S, Chang T, Tseng C, Chen L, Shih K;
XX
DR WPI; 2003-790112/75.
XX
PT Solid phase method, useful for synthesis of new peptide-spacer-lipid
PT conjugates, for incorporation into targeted therapeutic liposomes
PT containing therapeutic or diagnostic agents.
XX
PS Disclosure; Page 14; 29pp; English.

CC The present invention describes a solid phase method for the synthesis of
CC peptide-spacer-lipid conjugates, and targeted liposomes containing the
CC conjugates. The method comprises: (a) synthesising an amino acid residue
CC protected peptidyl resin in solid phase; (b) conjugating a spacer and a
CC lipid to the peptidyl resin; (c) cleaving the peptide-spacer-lipid from
CC the peptide-spacer-lipid resin; (d) removing at least one side chain
CC protecting group from at least one amino acid of the peptide-spacer
CC lipid, forming a peptide-spacer-lipid conjugate; and (e) subjecting the
CC conjugate to: (i) no further processing; (ii) modifying a peptide portion
CC of the conjugate to a cyclic form during any of steps (a)-(d) above; or
CC (iii) modifying a peptide portion of the conjugate to a cyclic form after
CC any of steps (a)-(d). The spacer is conjugated to each of the peptidyl
CC resin and the lipid by linkage functional groups, the 2 linkage
CC functional groups being the same or different. Also described: (1) a
CC peptide-spacer-lipid conjugate; and (2) a targeted therapeutic liposome
CC comprising a peptide-spacer-lipid conjugate, and optionally a therapeutic
CC agent for treating a disease or a diagnostic agent for diagnosing a

CC disease. The peptide-spacer-lipid conjugates have cytostatic activity,
CC and can be used as somatostatin receptor 2 inhibitors. The method is used
CC for the synthesis of peptide-spacer-lipid conjugates for incorporation
CC into targeted therapeutic liposomes containing therapeutic or diagnostic
CC agents, e.g. for targeted treatment of a somatostatin receptor expressed
CC cancer. The present sequence represents a fibroblast growth factor
CC peptide ligand used in the exemplification of the present invention.
XX
SQ Sequence 15 AA;

Query Match 25.0%; Score 35; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 13 SEISVGAEFNKDDC 26
| : ||| | : ||
Db 2 SALFVGAPFHVPDC 15

RESULT 3
ADJ56718
ID ADJ56718 standard; peptide; 15 AA.
XX
AC ADJ56718;
XX
DT 06-MAY-2004 (first entry)
XX
DE Fibroblast growth factor peptide ligand 1 of a peptide-lipid conjugate.
XX
KW FGF; fibroblast growth factor; solid phase synthesis;
KW peptide-spacer-lipid; peptide-PEG-lipid; liposome;
KW liposomal drug delivery; somatostatin receptor expressed cancer;
KW cytotstatic.
XX
OS Synthetic.
XX
PN US2003229017-A1.
XX
PD 11-DEC-2003.
XX
PF 03-DEC-2002; 2002US-00308644.
XX
PR 07-DEC-2001; 2001US-00016569.
XX
PA (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI Wu S, Chang T, Tseng C, Chen L, Shih K;
XX
DR WPI; 2004-178653/17.
XX
PT Solid phase synthesis of peptide-spacer-lipid conjugates useful for
PT synthesizing targeted therapeutic liposomes for treating or diagnosing a
PT disease e.g. cancer involves conjugating a spacer and a linker to a
PT peptidyl resin.
XX
PS Disclosure; Page 8; 20pp; English.

CC This invention relates to a novel solid phase synthesis method for
CC preparing peptide-spacer-lipid conjugates. Specifically, it refers to
CC preparing peptide-PEG-lipid conjugates and it provides the various
CC linkage groups (such as amide groups) required for such a conjugation.
CC The present invention describes an automated method for producing a wide
CC range of conjugates that is simple and minimises product loss during
CC synthesis. Furthermore, the peptide-spacer-lipid can be incorporated into
CC a liposome as the targeting moiety for liposomal drug delivery to
CC specific cells, and as such can be useful for the treatment and diagnosis
CC of certain diseases including somatostatin receptor expressed cancer.
CC Accordingly, these compositions exhibit cytostatic activity. This peptide
CC sequence is a peptide ligand component of a conjugate of the invention.
XX
SQ Sequence 15 AA;

Query Match 25.0%; Score 35; DB 8; Length 15;


```
Query Match      24.3%; Score 34; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 13 SEISVGAEFNKD 24
   ||: : ||| |
Db  7 SEVKIDAEFRHD 18

RESULT 6
AD016864
ID  ADO16864 standard; peptide; 19 AA.
XX  AC
AC  ADO16864;
XX  AC
DT  01-JUL-2004 (first entry)
XX  AC
DE  APP mutant peptide #3.
XX  AC
KW  Protease; caspase-induced apoptosis; proteolytic cleavage site; caspase;
KW  APP; mutant; mutein.
XX  AC
OS  Synthetic.
XX  AC
PN  US2004019529-A1.
XX  AC
PD  29-JAN-2004.
XX  AC
PF  28-MAY-2003; 2003US-00447655.
XX  AC
PR  20-OCT-1999; 99US-0160559P.
PR  16-AUG-2000; 2000US-0225664P.
PR  18-OCT-2000; 2000US-00691317.
XX  AC
PA  (LIYY/) LI Y.
PA  (CORD/) CORDELL B.
XX  AC
PI  Li Y, Cordell B;
XX  AC
DR  WPI; 2004-122025/12.
XX  AC
PT  Identifying inhibitors of a protease by providing a eukaryotic cell
PT  susceptible to caspase-induced apoptosis and isolating the cDNA
PT  expression vector that expresses the inhibitor from the eukaryotic cell
PT  that survives induction.
XX  AC
PS  Example 4; Fig 29A; 59pp; English.
XX  AC
CC  The invention relates to a method of identifying inhibitors of a
CC  protease, comprising providing a eukaryotic cell susceptible to caspase-
CC  induced apoptosis, where the eukaryotic cell expresses a gene encoding a
CC  protease and where the protease recognises a proteolytic cleavage site,
CC  introducing a fusion polypeptide expression vector into the eukaryotic
CC  cell, where the fusion polypeptide expression vector comprises an
CC  expression cassette encoding an inducible promoter that regulates a gene
CC  encoding a fusion polypeptide where the fusion polypeptide comprises an
CC  amino acid sequence for a first caspase subunit, a linker sequence and a
CC  second caspase subunit where the linker sequence comprises the
CC  proteolytic cleavage site, introducing a cDNA expression vector into the
CC  eukaryotic cell, where the cDNA expression vector expresses an inhibitor
CC  that inhibits the protease from cleaving the proteolytic cleavage site of
CC  the fusion polypeptide, inducing expression of the fusion polypeptide,
CC  isolating the eukaryotic cell after induction and isolating the cDNA
CC  expression vector that expresses the inhibitor from the eukaryotic cell
CC  that survives induction. The method is useful for identifying inhibitors
CC  of a protease. This sequence represents an APP mutant peptide used in the
CC  scope of the invention.
XX  AC
SQ  Sequence 19 AA;

Query Match      24.3%; Score 34; DB 8; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;

QY 13 SEISVGAEFNKD 24
   ||: : ||| |
Db  7 SEVKIDAEFRHD 18

RESULT 7
AAW35697
ID  AAW35697 standard; peptide; 20 AA.
XX  AC
AC  AAW35697;
XX  AC
DT  13-MAY-1998 (first entry)
XX  AC
DE  D. maculata antigen 5 peptide (residues 91-110).
XX  AC
KW  Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW  vespid venom; white face hornet wasp; immunodominant peptide; T cell.
XX  AC
OS  Synthetic.
XX  AC
PN  WO9733910-A1.
XX  AC
PD  18-SEP-1997.
XX  AC
PF  11-MAR-1997; 97WO-US003753.
XX  AC
PR  11-MAR-1996; 96US-00614935.
XX  AC
PA  (UYRQ ) UNIV ROCKEFELLER.
XX  AC
PI  King TP;
XX  AC
DR  WPI; 1997-470817/43.
XX  AC
PT  Vespid venom antigen 5 peptide fragments - useful to treat or diagnose
PT  vespid venom sensitivity.
XX  AC
PS  Example 1; Fig 2; 73pp; English.
XX  AC
CC  Sequences AAW35694-99 represent 15-20 residue peptides of white faced
CC  hornet antigen 5 molecule. The invention relates to peptides derived from
CC  vespid venom antigen 5 (VVS) that are antigenic for T cell proliferation
CC  in mice immunised with VVS. The peptides can be used to treat or diagnose
CC  vespid venom sensitivity e.g. to Dolichovespula maculata (white face
CC  hornet), Vespula vulgaris (yellowjacket), V. maculifrons (yellowjacket),
CC  D. arenaria (yellow hornet), Polistes amularis (wasp), P. exclamans
CC  (wasp), V. crabo (European hornet), V. flavopilosa (yellowjacket), V.
CC  germanica (yellowjacket), V. pennsylvanica yellowjacket), V. squamosa
CC  (yellowjacket), V. vidua (yellowjacket) and P. fuscatus (paperwasp)
XX  AC
SQ  Sequence 20 AA;

Query Match      24.3%; Score 34; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 20 EFNKDDC 26
   :||| |||
Db  5 DFNHDDC 11

RESULT 8
AAU77896
ID  AAU77896 standard; peptide; 20 AA.
XX  AC
AC  AAU77896;
XX  AC
DT  05-JUN-2002 (first entry)
XX  AC
DE  Bipla peptide tested for ability to block GD domain interactions.
```

XX GD domain; apoptosis; interaction with Bcl-XL; cell killing function;
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; bcl-2.
 XX Unidentified.
 XX US6221615-B1.
 XX 24-APR-2001.
 XX 25-JAN-1999; 99US-00236385.
 XX 12-MAY-1995; 95US-00440391.
 PR 08-AUG-1997; 97US-00908597.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX Chittenden TD, Lutz RJ;
 XX WPI; 2002-234950/29.
 XX Identifying agents (e.g. modulators of apoptosis) capable of modulating
 PT GD domain mediated heterodimerization or homodimerization comprises
 PT carrying out a heterodimerization or homodimerization assay.
 XX Disclosure; Col 6; 37pp; English.
 XX The present invention relates to novel peptides, designated GD domains,
 CC which are capable of modulating apoptosis. The GD domains are essential
 CC for Bak's interaction with Bcl-XL, and to Bak's cell killing function.
 CC The GD domains mediate key protein/protein interactions with multiple
 CC cell death regulatory molecules. Also described are methods of
 CC identifying agonists or antagonists of GD domains. The methods are useful
 CC for identifying agents capable of modulating GD domain mediated
 CC heterodimerization or homodimerization. The methods are particularly
 CC useful in drug screening and design, e.g. for identifying agents for
 CC treating autoimmune disease or cancer, or for identifying modulators of
 CC apoptosis. The present sequence represents a peptide tested for it's
 CC ability to block GD domain-mediated interactions
 XX Sequence 20 AA;
 SQ

Query Match 24.3%; Score 34; DB 5; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLGYHLDVSL 10
 Db 11 CIGDEMDVSL 20

RESULT 9
 ADK14728
 ID ADK14728 standard; peptide; 20 AA.
 AC ADK14728;
 XX 03-JUN-2004 (first entry)
 XX Bcl-2 related gene Bip-1a GD domain peptide seqid 41.
 XX anti-HIV; dermatological; immunosuppressive; antiinflammatory;
 KW antirheumatic; antiarthritic; GD domain peptide; apoptosis;
 KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;
 KW immunocrossreactive protein; degenerative disorder;
 KW cell proliferation disorder; cell death disorder; autoimmune disease;
 KW systemic lupus erythematosus; SLE; rheumatoid arthritis;
 KW acquired immunodeficiency syndrome; AIDS; Bip-1a.
 XX Unidentified.
 OS US2004054129-A1.
 XX

PD 18-MAR-2004.
 XX 10-APR-2001; 2001US-00828870.
 XX 12-MAY-1995; 95US-00440391.
 PR 08-AUG-1997; 97US-00908597.
 PR 25-JAN-1999; 99US-00236385.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX Chittenden TD, Lutz RJ;
 XX WPI; 2004-247780/23.
 XX Novel isolated and purified peptide comprising GD domain, useful for
 PT treating degenerative disease e.g., rheumatoid arthritis.
 XX Disclosure; SEQ ID NO 41; 38pp; English.
 XX The invention describes an isolated and purified peptide (I) comprising
 CC unrecognised protein domain (GD domain) isolated from the bcl-2 related
 CC gene Bak that can induce cell death. (I) is useful for identifying an
 CC agent capable of modulating GD domain radiated heterodimerisation or
 CC homodimerisation. (IV) is useful for screening a cDNA expression library
 CC for clones comprising DNA inserts encoding immunocrossreactive proteins
 CC (claimed). An anti-(I)-antibody, its mimetics, fragments, functional
 CC equivalents and/or hybrids or its mutants, and a vector comprising a
 CC polynucleotide encoding (I) are useful as agents for treating
 CC degenerative disorders including disorders having inappropriate cell
 CC proliferation or inappropriate cell death. The agents are also useful for
 CC treating disorders in which a cell is present and/or persists in an
 CC inappropriate location, and autoimmune disease such as systemic lupus
 CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder
 CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid
 CC sequence of a Bcl-2 family member Bip-1a GD domain peptide.
 XX Sequence 20 AA;
 SQ

Query Match 24.3%; Score 34; DB 8; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLGYHLDVSL 10
 Db 11 CIGDEMDVSL 20

RESULT 10
 AAW82186
 ID AAW82186 standard; peptide; 21 AA.
 XX AAW82186;
 XX 18-FEB-1999 (first entry)
 XX Fluorogenic protease indicator Swedish KM/NL AMLOID peptide #1.
 DE Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 XX conformation change.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 3 /label= Aib
 FT /note= "alpha-aminoisobutyric acid, labelled as amino
 FT acid B in the specification"
 FT Modified-site 4 /note= "epsilon-aminocaproic acid, labelled as amino acid
 FT J in the specification"
 FT Modified-site 16 /note= "epsilon-aminocaproic acid, labelled as amino acid
 FT J in the specification"

PT New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.

PS Disclosure; Page 27; 86pp; English.

XX The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention

XX Sequence 21 AA;

Query Match 24.3%; Score 34; DB 4; Length 21;

Best Local Similarity 53.3%; Pred. No. 3.1e+02;

Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 13 SEISVGAEFN--KDD 25

Db 6 SEVNLDAEFGCPKDD 20

||||: ||| |||

RESULT 13

ADN88519

ID ADN88519 standard; peptide; 21 AA.

XX AC ADN88519;

XX DT 12-AUG-2004 (first entry)

XX Fluorogenic protease indicator peptide #215.

XX fluorogenic; protease detection; protease inhibitor.

XX Synthetic.

XX US2004096926-A1.

XX 20-MAY-2004.

XX 04-JUN-2001; 2001US-00874350.

XX 20-FEB-1997; 97US-00802981.

XX 20-FEB-1998; 98WO-US003000.

XX 10-SEP-1999; 99US-00394019.

XX 11-SEP-2000; 2000WO-US024882.

XX (ONCO-) ONCOIMMUNIN INC.

XX Packard BS, Komoriya A;

XX WPI; 2004-399235/37.

XX Fluorogenic composition useful for detecting protease activity and test

XX substance modulating protease activity.

XX Claim 24; SEQ ID NO 215; 114pp; English.

XX The invention relates to a fluorogenic composition (I) for detecting the

XX activity of a protease. (I) is useful for detecting the activity of a

XX protease, which involves contacting the protease with (I), where the

XX activity of protease is detected in a histological section, cell culture

XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The

XX protease activity is detected by fluorescence microscopy, fluorescence

XX microplate reader, absorption microplate reader, flow cytometry,

XX reader. (I) is useful for delivering a molecule into a cell, and for

CC screening a test agent for the ability to modulate the activity of the
 CC protease. (I) is useful for detection and localisation of protease
 CC activity in biological samples. (I) also acts as a protease inhibitor,
 CC thus useful as protease inhibitors. (I) enables detection of the protease
 CC activity, and provides a high intensity fluorescent signal at a visible
 CC wavelength when they are digested by a protease. The present sequence
 CC represents a fluorogenic protease indicator peptide of the invention.

XX Sequence 21 AA;

Query Match 24.3%; Score 34; DB 8; Length 21;

Best Local Similarity 53.3%; Pred. No. 3.1e+02;

Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 13 SEISVGAEFN--KDD 25

Db 6 SEVNLDAEFGCPKDD 20

||||: ||| |||

RESULT 14

ADN88443

ID ADN88443 standard; peptide; 21 AA.

XX AC ADN88443;

XX DT 12-AUG-2004 (first entry)

XX Fluorogenic protease indicator peptide #139.

XX fluorogenic; protease detection; protease inhibitor.

XX Synthetic.

XX US2004096926-A1.

XX 20-MAY-2004.

XX 04-JUN-2001; 2001US-00874350.

XX 20-FEB-1997; 97US-00802981.

XX 20-FEB-1998; 98WO-US003000.

XX 10-SEP-1999; 99US-00394019.

XX 11-SEP-2000; 2000WO-US024882.

XX (ONCO-) ONCOIMMUNIN INC.

XX Packard BS, Komoriya A;

XX WPI; 2004-399235/37.

XX Fluorogenic composition useful for detecting protease activity and test

XX substance modulating protease activity.

XX Disclosure; SEQ ID NO 139; 114pp; English.

XX The invention relates to a fluorogenic composition (I) for detecting the

XX activity of a protease. (I) is useful for detecting the activity of a

XX protease, which involves contacting the protease with (I), where the

XX activity of protease is detected in a histological section, cell culture

XX or tissue section. The cell suspension is derived from the biological

XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The

XX protease activity is detected by fluorescence microscopy, fluorescence

XX microplate reader, absorption microplate reader, flow cytometry,

XX reader. (I) is useful for delivering a molecule into a cell, and for

XX screening a test agent for the ability to modulate the activity of the

XX protease. (I) is useful for detection and localisation of protease

XX activity in biological samples. (I) also acts as a protease inhibitor,

XX thus useful as protease inhibitors. (I) enables detection of the protease

XX activity, and provides a high intensity fluorescent signal at a visible

XX wavelength when they are digested by a protease. The present sequence

XX represents a fluorogenic protease indicator peptide of the invention.

SQ Sequence 21 AA;

Query Match 24.3%; Score 34; DB 8; Length 21;
Best Local Similarity 53.3%; Pred. No. 3.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 13 SEISVGAERN--KDD 25
|::: ||| |||
Db 6 SEVNLDAEFGXPKDD 20

RESULT 15

AAAY96324

ID AAAY96324 standard; peptide; 26 AA.

AC AAAY96324;

DT 17-AUG-2000 (first entry)

XX Mammalian Bik Bcl-2 homology domain 3 domain.

DE Mammal; apoptosis; cell death; BBC3; apoptosis promotion; Bik;

KW apoptosis inhibition; malignant cell; autoimmune disease.

XX OS

Mammalia.

XX WO2000026228-A1.

XX PD 11-MAY-2000.

XX PF 28-OCT-1999; 99WO-US025285.

XX PR 02-NOV-1998; 98US-00184168.

XX PA (CLON-) CLONTECH LAB INC.

XX PI Zhu L, Yin X, Chittenden T;

XX WPI; 2000-365560/31.

XX PT Novel polynucleotide encoding a BBC3 protein which is useful for
modulating apoptosis, especially in the treatment of cancer and
autoimmune diseases.

XX PS Disclosure; Fig 4; 47pp; English.

XX CC The present sequence is the mammalian Bik Bcl-2 homology domain 3 (BH3)
domain, which was used in a sequence alignment with the same domain of a
putative version of the mammalian apoptosis regulator BBC3, which was
designated BBC3-ORF2. The BBC3 protein, nucleic acids and antibodies are
suitable for use in promoting cell death or for preventing apoptosis in
malignant cells and those causing autoimmune diseases

XX SQ Sequence 26 AA;

Query Match 24.3%; Score 34; DB 3; Length 26;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLGYHLDVSL 10

|:|:| |

Db 11 CIGDEMDVSL 20

Search completed: June 8, 2005, 11:24:05
Job time : 160 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:27:01 ; Search time 150 Seconds
(without alignments)
66.445 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLARFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 362566

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	25.0	15	15	US-10-016-569A-13
2	35	25.0	15	15	US-10-308-644-13
3	34	24.3	18	17	US-10-816-698-12
4	34	24.3	18	17	US-10-816-698-13
5	34	24.3	20	11	US-09-828-870-41
6	34	24.3	21	10	US-09-747-287-172
7	34	24.3	21	11	US-09-747-287-173
8	34	24.3	21	11	US-09-874-350A-139
9	34	24.3	21	11	US-09-874-350A-215
10	33.5	23.9	25	14	US-10-083-357-1054
11	33	23.6	12	9	US-09-896-874-1

12	33	23.6	12	9	US-09-896-139-1	Sequence 1, Appli
13	33	23.6	12	9	US-09-895-843-1	Sequence 1, Appli
14	33	23.6	12	10	US-09-895-871-1	Sequence 3, Appli
15	33	23.6	12	15	US-10-400-273-3	Sequence 213, App
16	33	23.6	13	9	US-09-791-378-213	Sequence 223, App
17	33	23.6	13	9	US-09-791-378-223	Sequence 359, App
18	33	23.6	13	9	US-09-826-290-359	Sequence 372, App
19	33	23.6	13	10	US-09-826-290-372	Sequence 195, App
20	33	23.6	13	10	US-09-908-943A-195	Sequence 116, App
21	33	23.6	13	10	US-09-791-393-116	Sequence 213, App
22	33	23.6	13	11	US-09-791-377-213	Sequence 223, App
23	33	23.6	13	11	US-09-791-377-223	Sequence 350, App
24	33	23.6	13	15	US-10-264-309-350	Sequence 114, App
25	33	23.6	13	16	US-10-700-340-114	Sequence 195, App
26	33	23.6	13	16	US-10-801-487-195	Sequence 195, App
27	33	23.6	13	16	US-10-801-938-195	Sequence 195, App
28	33	23.6	13	16	US-10-801-509-195	Sequence 195, App
29	33	23.6	13	16	US-10-801-486-195	Sequence 195, App
30	33	23.6	13	17	US-10-801-493-195	Sequence 5, Appli
31	33	23.6	15	17	US-10-621-311-5	Sequence 65, Appli
32	33	23.6	20	15	US-10-427-208-65	Sequence 14, Appli
33	33	23.6	20	16	US-10-343-389A-14	Sequence 8, Appli
34	33	23.6	21	9	US-09-854-864-8	Sequence 8, Appli
35	33	23.6	21	9	US-09-855-158-8	Sequence 174, App
36	33	23.6	21	10	US-09-747-287-174	Sequence 175, App
37	33	23.6	21	10	US-09-747-287-175	Sequence 140, App
38	33	23.6	21	11	US-09-874-350A-140	Sequence 141, App
39	33	23.6	21	11	US-09-874-350A-141	Sequence 99, Appli
40	33	23.6	26	15	US-10-617-876-99	Sequence 510, App
41	33	23.6	26	15	US-09-573-822C-510	Sequence 512, App
42	32	22.9	10	10	US-09-573-822C-512	Sequence 514, App
43	32	22.9	10	10	US-09-573-822C-514	Sequence 2, Appli
44	32	22.9	10	10	US-09-573-822C-514	
45	32	22.9	12	9	US-09-896-874-2	

ALIGNMENTS

RESULT 1

US-10-016-569A-13
; Sequence 13, Application US/10016569A
; Publication No. US20030229013A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: P1379
; CURRENT APPLICATION NUMBER: US/10/016,569A
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Cell
US-10-016-569A-13

Query Match 25.0%; Score 35; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNKDDC 26

| : | | | |

Db 2 SALFVGAPFHVDC 15

RESULT 2

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US-10-308-644-13
; Sequence 13, Application US/10308644
; Publication No. US20030229017A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: P1379
; CURRENT APPLICATION NUMBER: US/10/308,644
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Cell
US-10-308-644-13

Query Match      25.0%; Score 35; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      13 SEISVGAEFNKDC 26
Db      2 SALFVGAPHPVDC 15
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RESULT 3
US-10-816-698-12
; Sequence 12, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-12

Query Match      24.3%; Score 34; DB 17; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLGYHLDVSL 10
      |.:|:|
Db      8 CIGDEMVDVSL 17
      |.:|:|

RESULT 4
US-10-816-698-13
; Sequence 13, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
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; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-13

Query Match      24.3%; Score 34; DB 17; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLGYHLDVSL 10
      |.:|:|
Db      7 CIGDEMVDVSL 16
      |.:|:|

RESULT 5
US-09-828-870-41
; Sequence 41, Application US/09828870
; Publication No. US20040054129A1
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/828,870
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/236,385
; FILING DATE: 25-JANUARY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; (C) ATTORNEY DOCKET NO. 104322.147CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 41
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 41
US-09-828-870-41

Query Match      24.3%; Score 34; DB 11; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CLGVHLDVSL 10
|:|:||||
Db 11 CIGDEMDVSL 20

RESULT 6

US-09-747-287-172
; Sequence 172, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-173

Query Match 24.3%; Score 34; DB 10; Length 21;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 13 SEISVGAEFN--KDD 25
|:|:|:||||
Db 6 SEVNLDAEFGXPKDD 20

RESULT 7

US-09-747-287-173
; Sequence 173, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 21

; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-173

Query Match 24.3%; Score 34; DB 10; Length 21;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 13 SEISVGAEFN--KDD 25
|:|:|:||||
Db 6 SEVNLDAEFGXPKDD 20

RESULT 8

US-09-874-350A-139
; Sequence 139, Application US/09874350A
; Publication No. US2004009626A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Aib
; NAME/KEY: MOD RES
; LOCATION: (16)..(16)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
US-09-874-350A-139

Query Match 24.3%; Score 34; DB 11; Length 21;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 13 SEISVGAEFN--KDD 25
|:|:|:||||
Db 6 SEVNLDAEFGXPKDD 20

RESULT 9
US-09-874-350A-215
; Sequence 215, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903840US
; CURRENT FILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 215
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-215

Query Match 24.3%; Score 34; DB 11; Length 21;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 13 SEISVGAEPN--KDD 25
|||::|||
Db 6 SEVNLDAEFCXPKDD 20

RESULT 10
US-10-083-357-1054
; Sequence 1054, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Qiangdong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REFERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 1054
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-1054

Query Match 23.9%; Score 33.5; DB 14; Length 25;
Best Local Similarity 42.9%; Pred. No. 5.4e+02;
Matches 9; Conservative 5; Mismatches 4; Indels 3; Gaps 1;

Qy 4 YHLDVSLAFSEISVGAEPNKD 24
|:|::|||
Db 2 YPLNLSIS---ISGGKETNRD 19

RESULT 11
US-09-896-874-1
; Sequence 1, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-1

Query Match 23.6%; Score 33; DB 9; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SEISVGAEPNK 23
|||::|||
Db 1 SEVNLDAEPRK 11

RESULT 12
US-09-896-139-1
; Sequence 1, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Preskots, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-1

Query Match 23.6%; Score 33; DB 9; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNK 23
| | | | |
Db 1 SEVNLDAEFRK 11

RESULT 13

US-09-895-843-1
; Sequence 1, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailleard, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-1

Query Match 23.6%; Score 33; DB 9; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNK 23
| | | | |
Db 1 SEVNLDAEFRK 11

RESULT 14

US-09-895-871-1
; Sequence 1, Application US/09895871
; Publication No. US20030096864A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Hom, Roy
; APPLICANT: John, Varghese
; APPLICANT: Mailleard, Michel
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.21USU1
; CURRENT APPLICATION NUMBER: US/09/895,871
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-871-1

US-09-895-871-1

Query Match 23.6%; Score 33; DB 10; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNK 23
| | | | |
Db 1 SEVNLDAEFRK 11

RESULT 15

US-10-400-273-3
; Sequence 3, Application US/10400273
; Publication No. US20040014194A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Brian
; APPLICANT: Hammond, Gerald S
; APPLICANT: Reichert, Paul
; APPLICANT: Strickland, Corey
; APPLICANT: Wang, Wenyan
; APPLICANT: Weber, Patricia C
; APPLICANT: Wong, Gwendolyn
; APPLICANT: Zhang, Lili
; TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND USING THE S
; FILE REFERENCE: J01531-K-US
; CURRENT APPLICATION NUMBER: US/10/400,273
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,937
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cleavage sequence
US-10-400-273-3

Query Match 23.6%; Score 33; DB 15; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SEISVGAEFNK 23
| | | | |
Db 2 SEVNLDAEFRK 12

Search completed: June 8, 2005, 11:40:07
Job time : 151 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 11:18:50 ; Search time 41 Seconds
(without alignments)
47.338 Million cell updates/sec

Title: US-09-020-393B-14_COPY_26_51

Perfect score: 140

Sequence: 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 221301

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	27.1	16	5 PCT-US94-07043A-1	Sequence 1, Appli
2	35	25.0	26	4 US-09-351-657A-36	Sequence 36, Appl
3	34	24.3	20	1 US-08-614-935-17	Sequence 17, Appl
4	34	24.3	20	3 US-09-130-287-17	Sequence 17, Appl
5	34	24.3	20	3 US-09-236-385A-41	Sequence 41, Appl
6	34	24.3	21	3 US-08-802-981-112	Sequence 112, App
7	33	23.6	21	2 US-08-659-984A-18	Sequence 18, Appl
8	33	23.6	21	3 US-08-802-981-113	Sequence 113, App
9	33	23.6	21	3 US-08-802-981-114	Sequence 114, App
10	33	23.6	21	3 US-08-660-531-18	Sequence 18, Appl
11	33	23.6	21	4 US-09-854-864-8	Sequence 8, Appli
12	32	22.9	22	2 US-08-313-200-8	Sequence 8, Appli
13	32	22.9	22	4 US-09-251-039-12	Sequence 12, Appl
14	31	22.1	19	1 US-08-324-301-3	Sequence 3, Appli
15	31	22.1	21	3 US-09-049-698-42	Sequence 42, Appl
16	30	21.4	13	2 US-08-706-741B-44	Sequence 44, Appl
17	30	21.4	13	2 US-08-924-695A-44	Sequence 44, Appl
18	30	21.4	15	1 US-08-440-391-7	Sequence 37, Appli
19	30	21.4	15	1 US-08-440-391-32	Sequence 32, Appl
20	30	21.4	15	2 US-08-248-839C-152	Sequence 152, App
21	30	21.4	15	2 US-08-908-597A-7	Sequence 7, Appli
22	30	21.4	15	2 US-08-908-597A-32	Sequence 32, Appl
23	30	21.4	15	3 US-09-236-385A-7	Sequence 7, Appli
24	30	21.4	15	3 US-09-236-385A-32	Sequence 32, Appl
25	30	21.4	15	5 PCT-US96-06122-7	Sequence 7, Appli
26	30	21.4	18	5 PCT-US96-06122-32	Sequence 32, Appl
27	30	21.4	18	5 PCT-US94-01234-21	Sequence 21, Appl

28 30 21.4 22 4 US-09-270-767-39259 Sequence 39259, A
29 30 21.4 22 4 US-09-270-767-54476 Sequence 54476, A
30 29.5 21.1 15 4 US-09-071-252-29 Sequence 29, Appl
31 29 20.7 8 4 US-09-535-852-1092 Sequence 1092, Ap
32 29 20.7 9 4 US-09-724-566A-88 Sequence 88, Appl
33 29 20.7 9 4 US-09-535-852-1093 Sequence 1093, Ap
34 29 20.7 9 4 US-09-471-669A-88 Sequence 88, Appl
35 29 20.7 10 4 US-09-535-852-1094 Sequence 1094, Ap
36 29 20.7 11 4 US-09-535-852-1095 Sequence 1095, Ap
37 29 20.7 15 4 US-09-239-043D-2146 Sequence 2146, Ap
38 29 20.7 15 4 US-09-239-043D-2201 Sequence 2201, Ap
39 29 20.7 15 4 US-09-239-043D-2220 Sequence 2220, Ap
40 29 20.7 16 3 US-09-171-705-41 Sequence 41, Appl
41 29 20.7 16 3 US-09-405-745-3 Sequence 3, Appli
42 29 20.7 20 4 US-08-978-277A-14 Sequence 14, Appl
43 29 20.7 24 1 US-08-461-597-4 Sequence 4, Appli
44 29 20.7 24 2 US-08-535-298-4 Sequence 4, Appli
45 29 20.7 24 5 PCT-US94-05569A-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
PCT-US94-07043A-1
; Sequence 1, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10889
; FILING DATE: November 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/880,914
; FILING DATE: May 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pamela A. Simonton
; REGISTRATION NUMBER: 31,060
; REFERENCE/DOCKET NUMBER: MTI 224.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-1

Query Match 27.1%; Score 38; DB 5; Length 16;
Best Local Similarity 53.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	13	SEISVGAEFNKDD	25
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RESULT 2

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US-09-351-657A-36
; Sequence 36, Application US/09351657A
; Patent No. 6545140
; GENERAL INFORMATION:
; APPLICANT: Harmon, Barry G.
; APPLICANT: Jackwood, Mark W.
; APPLICANT: Brockus, Charles W.
; TITLE OF INVENTION: DNA encoding an avian beta-defensin and uses thereof
; FILE REFERENCE: 757.007U.S1
; CURRENT APPLICATION NUMBER: US/09/351,657A
; CURRENT FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 60/092,668
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-351-657A-36

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Qy 4 YHLDVSLAFSEISVGAEFNK 23
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Db 4 HHLALLFLVLSAGSGFTQ 23

RESULT 3

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US-08-614-935-17
; Sequence 17, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; TITLE OF INVENTION: ANTIGEN 5
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-614-935-17

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Qy 20 EFNKDDC 26
: || || ||
Db 5 DFNHDDC 11

RESULT 4

US-09-130-287-17
US-09-130-287-17 Application US/09130287
; Sequence 17, Application US/09130287
; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; TITLE OF INVENTION: ANTIGEN 5
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-09-130-287-17

Qy 20 EFNKDDC 26


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; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-18

Query Match      23.6%; Score 33; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      13 SEISVGAEFNKD 24
Db      1 SEVNLDAEFRHD 12

RESULT 8
US-08-802-981-113
; Sequence 113, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; QUERY MATCH      23.6%; Score 33; DB 2; Length 21;
; BEST LOCAL SIMILARITY 50.0%; Pred. No. 96;
; MATCHES 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      13 SEISVGAEFN--KDD 25
Db      6 SEVKLDAEFGPKDD 20

RESULT 9
US-08-802-981-114
; Sequence 114, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; QUERY MATCH      23.6%; Score 33; DB 3; Length 21;
; BEST LOCAL SIMILARITY 53.3%; Pred. No. 96;
; MATCHES 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY      13 SEISVGAEFN--KDD 25
Db      6 SEVKLDAEFGPKDD 20

RESULT 9
US-08-802-981-114
; Sequence 114, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; QUERY MATCH      23.6%; Score 33; DB 3; Length 21;
; BEST LOCAL SIMILARITY 53.3%; Pred. No. 96;
; MATCHES 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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QY      13 SEISVGAEFN--KDD 25
      ||: . ||| |||
Db      6 SEVNDAEFGXPKDD 20

RESULT 10
US-08-660-531-18
; Sequence 18, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-18

Query Match      23.6%; Score 33; DB 3; Length 21;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      13 SEISVGAEFNKD 24
      ||: . ||| |||
Db      1 SEVNLDAEPRHD 12

RESULT 11
US-09-854-864-8
; Sequence 8, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
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; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-8

Query Match      23.6%; Score 33; DB 4; Length 21;
Best Local Similarity 53.8%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CLGYHLDVSLA 11
      ||| | |||
Db      5 CLGSLIISLA 15

RESULT 12
US-08-313-200-8
; Sequence 8, Application US/08313200
; Patent No. 5998153
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,200
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20658.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-200-8

Query Match      22.9%; Score 32; DB 2; Length 22;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      13 SEISVGAEFNK 23
      ||: . ||| |||
Db      10 SRLDTGAEINLK 20

RESULT 13
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US-09-251-039-12
; Sequence 12, Application US/09251039
; Patent No. 6528059
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; APPLICANT: University of Michigan
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; FILE REFERENCE: 203442065801
; CURRENT APPLICATION NUMBER: US/09/251,039
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/313,200
; EARLIER FILING DATE: 1994-11-08
; EARLIER APPLICATION NUMBER: 07/885,656
; EARLIER FILING DATE: 1992-05-19
; EARLIER APPLICATION NUMBER: PCT/US93/03837
; EARLIER FILING DATE: 1993-04-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown
; US-09-251-039-12

Query Match      22.9%; Score 32; DB 4; Length 22;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      13 SEISVGAEFNK 23
DB      10 SRLDTGAELNK 20

RESULT 14
US-08-324-301-3
; Sequence 3, Application US/08324301
; Patent No. 5597569
; GENERAL INFORMATION:
; APPLICANT: Siegal, Clay B.
; APPLICANT: Gawlak, Susan L.
; APPLICANT: Marquardt, Hans
; TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
; TITLE OF INVENTION: ISOLATED FROM THE PLANT BRYONICA DIOICA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,301
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,891
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0109A
; TELEPHONE: 206-728-4800
; TELEFAX: 206-727-3601
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6368792e
; US-09-049-698-42

US-09-251-039-12
; Sequence 12, Application US/09251039
; Patent No. 6528059
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; APPLICANT: University of Michigan
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; FILE REFERENCE: 203442065801
; CURRENT APPLICATION NUMBER: US/09/251,039
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/313,200
; EARLIER FILING DATE: 1994-11-08
; EARLIER APPLICATION NUMBER: 07/885,656
; EARLIER FILING DATE: 1992-05-19
; EARLIER APPLICATION NUMBER: PCT/US93/03837
; EARLIER FILING DATE: 1993-04-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown
; US-09-251-039-12

Query Match      22.1%; Score 31; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 DVSLAFSEIS 16
DB      2 NIELGFSEIS 11

RESULT 15
US-09-049-698-42
; Sequence 42, Application US/09049698
; Patent No. 6368792
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA A.
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
; TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,856
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6068.US.PI
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-3623
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6368792e
; US-09-049-698-42
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Query Match 22.1%; Score 31; DB 3; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 15 ISVGAEPFKD 24
|:|:|
Db 8 ITVNAKMKD 17

Search completed: June 8, 2005, 11:28:25
Job time : 42 secs

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